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14. ABSTRACT The proposal was designed to address three issues. First could we identify stem cells from the fallopian tube, including from patients with high grade serous cancer (HGSC). Second, could we link the molecular abnormalities in cancer associated stem cells and validate them in pathologic material, specifically in what we feel are stem cell outgrowths or SCOUTs and third could we identify molecular alterations that would place the oviduct or the patient at risk for HGSC. In essence we wished to drill down to the cell of origin and link it to cancer risk, identifying an assay that could predict the presence of cancer by analyzing lower genital tract fluids or other samples.						
15. SUBJECT TERMS HGSC = high grade serous cancer; Fallopian tube; BRCA; Tp53, SCOUT = stem cell outgrowth; STIC = serous tubal intraepithelial carcinoma; STIN = serous tubal intraepithelial neoplasia.						
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1. INTRODUCTION: The proposal was designed to address three issues. First could we identify stem cells from the fallopian tube, including from patients with high grade serous cancer (HGSC). Second, could we link the molecular abnormalities in cancer associated stem cells and validate them in pathologic material, specifically in what we feel are stem cell outgrowths or SCOUTs and third could we identify molecular alterations that would place the oviduct or the patient at risk for HGSC. In essence we wished to drill down to the cell of origin and link it to cancer risk, identifying an assay that could predict the presence of cancer by analyzing lower genital tract fluids or other samples.

KEYWORDS: HGSC = high grade serous cancer ; Fallopian tube; BRCA; Tp53, SCOUT = stem cell outgrowth; STIC = serous tubal intraepithelial carcinoma; STIN = serous tubal intraepithelial neoplasia.

2. ACCOMPLISHMENTS: All three goals were addressed in the past year with some modifications that will be addressed under part 5.

What were the major goals of the project?

The specific aims were as follows:

AIM 1: To grow stem cells from the tubes in culture from patients with and without malignancy and compare them.

AIM 2: Link the molecular disturbances seen in cancer associated stem cells and validate them in pathologic material specifically an entity we have described called the stem cell outgrowth or SCOUT.

AIM 3: Exploit the molecular alterations to make molecular probes that will detect those alterations that place women at risk for the disease, either in the fallopian tubes or lower genital tract fluids.

What was accomplished under these goals?

AIM 1: 1) Major activity: grow and identify fallopian stem cells in culture. 2) The specific objective was to identify stem cell characteristics that distinguished tumor associated (but normal appearing) stem cells from normal controls. 3) Significant results: a) We successfully cloned stem cells from normal fallopian tubes and showed that these cells were capable of both ciliated and squamous differentiation, in parallel with the histology of the fallopian tube (Figure 1). b) We generated a "stem cell" specific signature by comparing gene expression between undifferentiated stem cells and those grown on an air-liquid interface, which permitted ciliated differentiation. This was the first ever successful cloning, propagation and maturation of fallopian tube stem cells (Ning et al 2015). What we have not accomplished is to show that stem cells from normal tubal epithelium in cancers can be distinguished from epithelium from normal controls. b) An additional achievement, however, was to identify potential stem cell markers that were novel and might be used to unearth potential stem cells in the general pool of non-ciliated tubal epithelium (Yamamoto et al 2015). Moreover, we showed remarkable parallels between stem cells and putative stem cell outgrowths as well as HGSC precursors. c) Another added achievement was to demonstrate a parallel between immortalized and transformed stem cells and precursor and malignant HGSCs in the fallopian tube (Figures 2&3). D) Still another added achievement was a successful experiment focusing on propagating potential cancer stem cells. In this study we identified subpopulations that were Taxane resistant and were able to identify the same cells in Taxane naive cell cultures (Ning et al, submitted). This suggests that there is a small population of chemo-resistant cells that is inborn and not created by chemotherapy per se.

AIM 2 1) Major activity: Translating the *in vitro* findings to histopathology. 2) Objective : To link the disturbances in cancer associated stem cells and validate them in pathologic material. 3) Significant results: Although we have not yet shown that stem cells in cancer-associated tubes differ from normal, the expression profile of normal stem

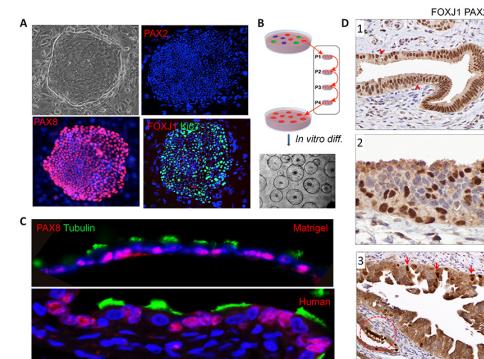


Figure 1. In-vivo propagation of fallopian tube stem cells with tissue correlates (See Ning 2015).

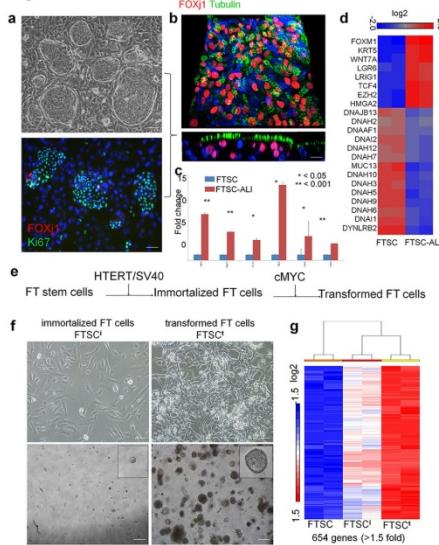


Figure 2. Upper panels show demonstrate differences in expression between putative stem cells and cell undergoing ciliated differentiation in vitro. Lower panel depicts progressive change of gene expression among FTSC, and immortalized and transformed FTSCs (See Yamamoto 2015).

HGSC. Third, we recently sequenced cases with bilateral STICs and have shown them to contain *identical* p53 mutations. This raises the critical question that not all STICs develop *de novo* but may signify mucosal metastases from either the opposite tube or another site (Meserve et al unpublished). Fourth, we have concluded the preliminary phase of an ambitious project that has exhaustively analyzed fallopian tubes of women with HGSC.

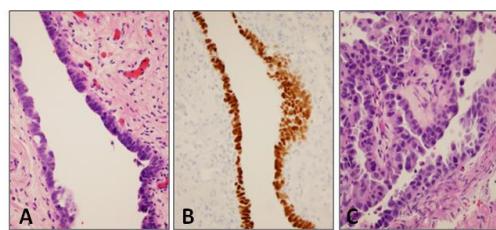


Figure 4. Mild tubal atypia (A) associated staining for p53 (B) is associated with a pelvic HGSC (C). Both lesions shared the same Tp53 mutation.

indicate the presence of an upper genital tract neoplasm. Significant results: We decided to use a novel approach to this problem by first identifying cases of HGSC and then searching the archive for prior formalin-fixed, paraffin embedded endometrial specimens from diagnostic procedures. DNA from serial sections of this material was extracted and then analyzed on a platform targeting p53 mutations. These mutations were compared to those found in the tumors at a later date. We identified 5 samples in which information was available. In two (40%) we detected p53 mutation in prior endometrial samples that matched those found in the subsequent tumor (Figure 5). The intervals from detecting the mutations to the diagnosis of the tumors were 2 weeks and 2 months.

cells closely resembles what we are seeing in so-called stem cell outgrowths (SCOUTs) as well as serous cancer precursors (STICs). This was shown in the papers by Ning et al and Yamamoto et al. Additional achievements: During these studies we took the opportunity to address an issue fundamental to the aims, which is the origin of HGSC. Because a high grade precancerous process (or STIC) can only be uncovered in subset of cancers, we felt it important to address this issue, the goal being to better understand the potential origins of these neoplasms. This was done in series of studies. First, we showed a potential dualistic model for HGSC with a lower association with STIC seen for tumors with certain morphologic features (Howitt 2015). This suggests that there could be more than one pathway to HGSC including one where STIC is not the

primary predecessor. Second, we showed that certain histologic patterns were associated with specific gene mutations (Ritterhouse et al submitted) again suggesting more than one pathogenetic route to

HGSC. Third, we recently sequenced cases with bilateral STICs and have shown them to contain *identical* p53 mutations. This raises the critical question that not all STICs develop *de novo* but may signify mucosal metastases from either the opposite tube or another site (Meserve et al unpublished). Fourth, we have concluded the preliminary phase of an ambitious project that has exhaustively analyzed fallopian tubes of women with HGSC but no STIC. In these tubes we have seen non-cancerous epithelium with p53 mutations. On comparing the p53 mutations status between these non-cancerous epithelia and the associated (and physically removed) HGSCs we have discovered *identical* mutations. This suggests the possibility that pelvic HGSCs could be derived from minor atypias within genetically altered stem cell proliferations (Figure 4). This has potentially profound implications in that it suggests that the serous carcinogenic sequence can initiate in the tube but continue beyond the confines of the oviduct at an unknown pelvic location (Soong et al unpublished).

AIM3: 1) Major activity: To develop a means to detect the presence of biomarkers unique to serous cancer or serous cancer risk in the uterus or lower genital tract. Objective: To employ second generation sequencing (deep sequencing) to identify p53 mutations in the lower genital tract tissues or fluids that would

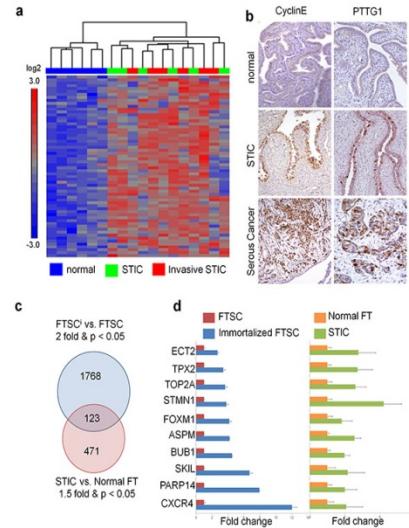


Figure 3. Overlapping gene expression between immortalized fallopian tube stem cells and serous carcinoma (See Yamamoto 2015).

What opportunities for training and professional development has the project provided?

This project has provided extensive training opportunities. Dr. Brooke Howitt, a co-investigator, is a junior attending (instructor) who was actively involved in study design and execution. Moreover, she was engaged in project planning with four resident/fellows (Kyle Strickland, Lauren Ritterhouse, Emily Meserve, Rinda Soong) and supervised them on these projects. Fellows were introduced to DNA extraction, data analysis, second generation sequencing etc. and three are interested in a career in academic gynecologic pathology. All of these individuals have presented their data at the USCAP meeting (in Boston in 2015) and/or have abstracts submitted on the above projects to the USCAP meeting scheduled for Seattle in 2016. They also will present their results in a departmental seminar scheduled for February 2016. The list of abstracts presented and planned is below.

The contributions of two additional members of the team were supported partially by this grant. The first was a summer college (From Washington University) student, Brennan Beeler, who is planning a career in research. A second is a Danish medical student taking a year off for research, Helena Dietzel. She has been working closely with Dr. Howitt, creating an important opportunity for Ms Dietzel as well as for Dr. Howitt to mentor a younger colleague.

How were the results disseminated to communities of interest?

The PI has participated in an outreach program to disseminate information on ovarian cancer.

(http://www.brighamandwomens.org/Departments_and_Services/obgyn/Services/ovarian-cancer-treatment.aspx)

Dr. Howitt has spent time in both Rwanda and Haiti performing outreach activities in the past year.

What do you plan to do during the next reporting period to accomplish the goals?

For year two the following projects are planned.

AIM1: We have a series of stem cell markers that have been unearthed by the in vitro comparison of FTSCs and FTSCs in an air-liquid interface. The protein atlas will be surveyed and 20 candidates will be identified and used to probe normal fallopian tube mucosa. We will focus primarily on markers that overlap in the same cells or region in an effort to find a consistently reproducible putative stem cell signature. Once we accomplish this we will do the following: 1) Map the distribution of putative stem cells in the fallopian tube as a function of location and age including reproductive status. The goal will be to determine if putative stem cells concentrate in particular areas of the fallopian tube and whether their distribution and frequency are altered by factors such as hormones, pregnancy, and menopause. 2) Confirm the presence of stem cell markers in lesions at variable stages of serous carcinogenesis. This will entail analysis of p53 signatures, tubal intraepithelial neoplasms and STICs.

AIM2: We are going to further explore the concept that early atypias in the fallopian tube are capable of spreading to the peritoneum. Our plan will be to analyze 25 cases of HGSC with negative fallopian tubes and concentrate on identifying early p53 mutations signatures that can be linked to HGSC. To accomplish this we will 1) microdissect non-malignant p53 positive clonal expansions in the tube and determine the nature of their mutations by next generation sequencing. The mutations will be compared to those of the concurrent serous carcinomas. 2) We will compare this group with 25 cases of HGSC associated with STICs that co-exist with less marked atypias, i.e. STICs most likely to represent primary tubal precursors. The goal will be to determine if BRCA status, the age of tumor presentation and distribution of tumor between the two groups highlights important differences.

AIM3: We will further expand the concept that archival material can be probed for p53 mutations to predict the presence of an intraabdominal HGSC. We will expand the pilot to 30 cases of HGSC that were preceded by a normal curetting and assess both HGSC and the prior material for matching mutations. This will be accomplished by next generation sequencing.

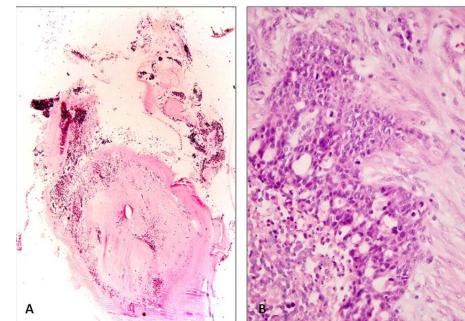


Figure 5. (A) An endometrial sample contains mostly mucus and a few cells. Extracted DNA from this archival sample revealed a p53 mutation identical to that found in a HGSC diagnosed over 2 months later.

4. IMPACT: The PI and his colleagues were the first to provide solid evidence that a high percentage of high-grade serous carcinomas (HGSC) in the pelvis arise in the fallopian tube. This work began in 2005 and has been associated with a paradigm shift in this field. A testimony to the extent and speed of this evolution can be seen in the sudden increase in programs targeting the fallopian tube and funding opportunities (many from the DOD) that have been placed on this conceptual framework. This pilot project was designed specifically to address the concept that there is an underpinning of unique stem cell biology that confers risk of HGSC. If such is true, we would expect to see unique differences between normal tubes associated with HGSCs and controls. We have yet to answer this particular question but we have made major advances in our understanding of the stem cell populations in the fallopian tube, which is a necessary prerequisite to any such endeavors. Taking into account the additional studies supported by this pilot, the areas of potential impact can be summarized as follows.

Impact on the principle and other disciplines

1. Stem cell biology: If we assume that stem cells are the vulnerable targets in serous carcinogenesis we must identify them and then determine if their numbers are increased in patients with cancer and map their distribution in the fallopian tubes throughout reproductive and postmenopausal life. The recent papers by Ning et al and Yamamoto et al provide the research community ("the principle discipline") with abundant evidence for further development of this concept. Other disciplines have clearly received benefit as evidenced by the parallel studies performed in the pulmonary and gastrointestinal tract by our collaborators Wa Xian and Frank McKeon. This concept of "stem cell" has been re-named "ground state" cells in their studies.

2. The origins of HGSC: The additional projects that query the role of the fallopian tube in the genesis of a serous carcinogenic sequence are vital to our understanding of where these tumors come from. The questions we pose are STICs really a primary process or an intramucosal metastasis and are we overestimating the importance of STICs? and is there some other source of HGSC that we need to understand before we pursue prophylactic salpingectomy? It is highly likely that not all STICs are primary tubal neoplasm (i.e. they could in some instances represent tumor that migrates from another site) but this re-emphasized the need to determine where in the carcinogenic sequence that *tumorigenesis* initiates. The general assumption is that STICs develop and then invade or spread to pelvic surfaces. Another possibility is that altered stem cells invade or spread prior to becoming STICs and emerge suddenly in an *extra-ovarian* site. We have initiated studies to answer both of these questions and the answers to both are germane to the notion that prophylactic salpingectomy will have the desired effect of preventing HGSC.

3. The potential discovery of gene mutations in archival material prior to the onset of HGSC: We have preliminary data that supports the possibility that the simple screening of an archival specimen will detect mutations that indicate the presence of an undiagnosed HGSC. The degree to which this will interrupt the natural history of this disease remains unclear but it adds to emerging data indicating that early diagnosis of HGSC is possible by analyzing routine specimens from the lower genital tract.

What was the impact on technology transfer?

Nothing to report

What was the impact on society beyond science and technology?

2. Origins of HGSC: The management of women with germ-line mutations in BRCA1 and BRCA2 is in a state of flux as the question remains as to the degree of benefit that can be expected from prophylactic salpingo-oophorectomy. This population has been keenly aware of the data emerging in this field and is making decisions about cancer prevention around the concept that most of these tumors could originate from the fallopian tube.

3. The potential discovery of gene mutations in archival material prior to the onset of HGSC: Any lay person can imagine the potential value of a test for ovarian cancer that can be applied to their endometrial biopsy.

5. CHANGES/PROBLEMS:

Changes in the direction and scope of the projects

AIM 1: No significant changes. The original goal was to identify alterations in fallopian tube stem cells that distinguish tubes associated with HGSCs from those of control fallopian tubes. We did not demonstrate this in the data obtained so far but we have identified a stem-cell signature (albeit one that will require pruning). While it is unlikely that we will identify differences in stem cell between cancer associated and control tubes, we have the tools to more precisely morphologically define stem or "ground state" cells in the tube. If we accomplish this then we can determine whether these cells are in greater abundance in the fimbria. If not we will be positioned to retrieve genetic information from these disparate stem cell populations and search for factors that influence stem cell vulnerability. No delays or problems are anticipated and there will be no change in expenditures.

AIM2: We have succeeded in translating in vitro fallopian tube stem cells to histopathology for the most part. We will plan to shift our emphasis to address whether early precursor lesions that emerge from these stem cell are able to initiate a progression sequence to HGSC in or beyond the tube. There will be no delays or human subject issues. We do however anticipate some increase in costs that were incurred in the first year of funding. Because of the exhaustive sampling of multiple fallopian tubes to unearth the small foci suspected of being precursors to HGSC we have incurred considerable costs for tissue sectioning.

AIM3: This is essentially unchanged other than the novel approach to detecting mutations in *archival* material. This material is readily available and we anticipate no changes in cost.

Changes in funding for which we are requesting approval

No changes in funding are anticipated.

6. PRODUCTS: List any products resulting from the project during the reporting period. Examples of products include:

Publications

Yamamoto Y, Ning G, Howitt BE, Mehra K, Wu L, Wang X, Hong Y, Kern F, Wei TS, Zhang T, Nagarajan N, Basuli D, Torti S, Brewer M, Choolani M, McKeon F, Crum CP, Xian W. In Vitro and In Vivo Correlates of Physiologic and Neoplastic Human Fallopian Tube Stem Cells. *J Pathol*. 2015 Sep 28. [Epub ahead of print]

Novak M, Lester J, Karst AM, Parkash V, Hirsch MS, Crum CP, Karlan BY, Drapkin R. Stathmin 1 and p16INK4A are sensitive adjunct biomarkers for serous tubal intraepithelial carcinoma. *Gynecol Oncol*. 2015 Jul 20.. [Epub ahead of print]

Worley MJ Jr, Liu S, Hua Y, Kwok JS, Samuel A, Hou L, Shoni M, Lu S, Sandberg EM, Keryan A, Wu D, Ng SK, Kuo WP, Parra-Herran CE, Tsui SK, Welch W, Crum C, Berkowitz RS, Ng SW. Molecular changes in endometriosis-associated ovarian clear cell carcinoma. *Eur J Cancer*. 2015 Sep;51(13):1831-42.

Wang X, Yamamoto Y, Wilson LH, Zhang T, Howitt BE, Farrow MA, Kern F, Ning G, Hong Y, Khor CC, Chevalier B, Bertrand D, Wu L, Nagarajan N, Sylvester FA, Hyams JS, Devers T, Bronson R, Lacy DB, Ho KY, Crum CP, McKeon F, Xian W. Cloning and variation of ground state intestinal stem cells. *Nature*. 2015 Jun 11;522(7555):173-8.

Ianova A, Loo A, Tworoger S, Crum CP, Fan I, McLaughlin JR, Rosen B, Risch H, Narod SA, Kotsopoulos J. Ovarian cancer survival by tumor dominance, a surrogate for site of origin. *Gynecol Oncol*, in press.

Howitt BE, Hanamornroongruang S, Lin DI, Conner JE, Schulte S, Horowitz N, Crum CP, Meserve EE. Evidence for a Dualistic Model of High-grade Serous Carcinoma: BRCA Mutation Status, Histology, and Tubal Intraepithelial Carcinoma. *Am J Surg Pathol*. 2015 Mar;39(3):287-93. PMID:25581732

Zuo W, Zhang T, Wu DZ, Guan SP, Liew AA, Yamamoto Y, Wang X, Lim SJ, Vincent M, Lessard M, Crum CP, Xian W, McKeon F. p63(+)Krt5(+) distal airway stem cells are essential for lung regeneration. *Nature*. 2015 Jan 29;517(7536):616-20. PMID:25383540

Ning G, Bijron JG, Yamamoto Y, Wang X, Howitt BE, Herfs M, Yang E, Hong Y, Cornille M, Wu L, Hanamornroongruang S, McKeon FD, Crum CP, Xian W. The PAX2-null immunophenotype defines multiple lineages with common expression signatures in benign and neoplastic oviductal epithelium. *J Pathol*. 2014 Dec;234(4):478-87. PMID:25130537

Books or non-periodical publications

Berek JS, Crum C, Friedlander M. Cancer of the ovary, fallopian tube, and peritoneum. *Int J Gynaecol Obstet*. 2015 Oct;131 Suppl 2:S111-22.

Poole EM, Rice MS, Crum CP, Tworoger SS. Salpingectomy as a potential ovarian cancer risk-reducing procedure. *J Natl Cancer Inst*. 2015 Jan 27;107(2). PMID:25628373

Kaspar HG, Crum CP. The utility of immunohistochemistry in the differential diagnosis of gynecologic disorders. *Arch Pathol Lab Med*. 2015 Jan;139(1):39-54. PMID:25549143 Review

Presentations, conference publications

Past presentations

Jelena Mirkovic, Amy DiVasta, Stacey Missmer, Brooke Howitt, Christopher Crum, Marc Laufer, Sara Vargas. The Histologic Spectrum of Adolescent Endometriosis. USCAP meeting, Boston, March 2015

Andre Pinto, Brooke Howitt, Christopher Crum. The Variable Spectrum of Tubal Intraepithelial Neoplasia in Women With High Grade Serous Carcinoma. USCAP meeting, Boston, March 2015

Lauren Ritterhouse, Christopher Crum, Lynette Sholl, Neal Lindeman, Brooke Howitt. Morphologic and Molecular Evaluation of Extra-Uterine Mullerian Carcinoma. USCAP meeting, Boston, March 2015

Submitted presentations for the USCAP 2016 meeting

Kyle C Strickland, Emily Meserve, Helena M Ditzel, Frank Campbell , Alexander Miron, Christopher P Crum, and Brooke E Howitt. Detection of Tumor Specific TP53 Signatures from Archival Endometrial Biopsies Prior to the Diagnosis of HighGrade Serous Carcinoma.

Emily E Meserve, Alexander Miron, Helena Ditzel, Andre Pinto, Frank Campbell, Brooke E Howitt, Christopher P Crum. Identical TP53 mutation in “bilateral” serous tubal intraepithelial carcinoma (STIC)

Emily E Meserve, Jelena Mirkovic, James R Conner , Eric Yang, Brooke E Howitt, Christopher P Crum. Detection of serous tubal intraepithelial carcinoma (STIC) in incidentally removed fallopian tubes from low-risk women.

Thing Rinda Soong, Christopher P Crum, Brooke E Howitt. Serial Sectioning of Distal Fallopian Tubes and its Role in the Discovery of Occult Serous Tubal Intraepithelial Carcinoma in Women with High Grade Ovarian Serous Carcinoma.

7. PARTICIPANTS & OTHER COLLABORATING ORGANIZATIONS

Individuals who worked on the project

Collaboration with Wa Xian at the Jackson Laboratory: We have a long-standing collaboration with Wa Xian who was at the Jackson Laboratory the past year. Her group received de-identified specimens for cell culture under an IRB approved protocol (included). Her laboratory was funded by the Jackson Laboratory and she did not receive

funds from this grant. She has now moved to the University of Texas at Houston. We are currently not sending specimens pending the approval of an MTA, after which an amendment will be issued to the IRB.

Changes in active other support of the PD/PI(s) or senior/key personnel since the last reporting period?

None

What other organizations were involved as partners?

Nothing to report.

8. SPECIAL REPORTING REQUIREMENTS: None

9. APPENDIX:

Selected Manuscripts:

Yamamoto Y, Ning G, Howitt BE, Mehra K, Wu L, Wang X, Hong Y, Kern F, Wei TS, Zhang T, Nagarajan N, Basuli D, Torti S, Brewer M, Choolani M, McKeon F, Crum CP, Xian W. In Vitro and In Vivo Correlates of Physiologic and Neoplastic Human Fallopian Tube Stem Cells. *J Pathol*. 2015 Sep 28. [Epub ahead of print]

Wang X, Yamamoto Y, Wilson LH, Zhang T, Howitt BE, Farrow MA, Kern F, Ning G, Hong Y, Khor CC, Chevalier B, Bertrand D, Wu L, Nagarajan N, Sylvester FA, Hyams JS, Devers T, Bronson R, Lacy DB, Ho KY, Crum CP, McKeon F, Xian W. Cloning and variation of ground state intestinal stem cells. *Nature*. 2015 Jun 11;522(7555):173-8.

Howitt BE, Hanamornroongruang S, Lin DI, Conner JE, Schulte S, Horowitz N, Crum CP, Meserve EE. Evidence for a Dualistic Model of High-grade Serous Carcinoma: BRCA Mutation Status, Histology, and Tubal Intraepithelial Carcinoma. *Am J Surg Pathol*. 2015 Mar;39(3):287-93. PMID:25581732

Ning G, Bijron JG, Yamamoto Y, Wang X, Howitt BE, Herfs M, Yang E, Hong Y, Cornille M, Wu L, Hanamornroongruang S, McKeon FD, Crum CP, Xian W. The PAX2-null immunophenotype defines multiple lineages with common expression signatures in benign and neoplastic oviductal epithelium. *J Pathol*. 2014 Dec;234(4):478-87. PMID:25130537



In Vitro and In Vivo Correlates of Physiologic and Neoplastic Human Fallopian Tube Stem Cells

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Tissue:	
Pathology:	
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Manuscripts

1
2
3 ***In Vitro and In Vivo Correlates of Physiologic and Neoplastic Human Fallopian***
4 ***Tube Stem Cells***
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6
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8 Yusuke Yamamoto^{1,10*}, Gang Ning^{1,10}, Brooke E. Howitt², Karishma Mehra², Lingyan
9 Wu³, Xia Wang¹, Yue Hong¹, Florian Kern³, Tay Seok Wei³, Ting Zhang³, Niranjan
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Abstract

High-grade serous cancer (HGSC) progresses to advanced stages without symptoms and the 5-year survival rate is a dismal 30%. Recent studies of ovaries and fallopian tubes in patients with BRCA1 or BRCA2 mutations have documented a pre-metastatic intramucosal neoplasm that is found almost exclusively in the fallopian tube termed "serous tubal intraepithelial carcinoma" or STIC. Moreover, other proliferations, termed p53 signatures, secretory cell outgrowths (SCOUTs) and lower grade serous tubal intraepithelial neoplasms (STINs) fall short of STIC but share similar alterations in expression, in keeping with an underpinning of genomic disturbances involved in - or occurring in parallel with serous carcinogenesis. To gain insight into the cellular origins of this unique tubal pathway to high-grade serous cancer, we cloned and both immortalized and transformed fallopian tube stem cells (FTSC). We demonstrated that pedigrees of FTSCs were capable of multi-potent differentiation and that the tumors derived from the transformed FTSC shared the same histological and molecular features with HGSC. We also demonstrated that altered expression of some biomarkers seen in transformed FTSCs and HGSCs (Stathmin, EZH2, CXCR4, CXCL12 and FOXM1) could be seen as well in immortalized cells and their *in vivo* counterparts SCOUTs and STINs. Thus, a whole-genome transcriptome analysis comparing FTSC, immortalized FTSC, and transformed FTSC showed a clear molecular progression sequence that is recapitulated by the spectrum of accumulated perturbations characterizing the range of proliferations seen *in vivo*. Biomarkers unique to STIC relative to normal tubal epithelium provide a basis for novel detection approaches to early HGSC, but must be viewed critically given their potential expression in lesser proliferations. Perturbations shared by both immortalized and transformed FTSCs may provide unique early targets for prevention strategies. Central to these efforts has been the ability to clone and perpetuate multi-potent FTSCs.

10 11 **Introduction**

12 Epithelial ovarian cancer (EOC) is the fifth most common cause of death from
13 cancer in women, and the most common type – high grade serous carcinoma or HGSC
14 – is the most lethal. One in 200 women will develop ovarian cancer between their 50th
15 and 70th birthday. Worldwide, there are 225,000 new cases of ovarian cancer diagnosed
16 annually, and an estimated 140,163 disease-related deaths¹. Up to 80% of women
17 present with Stages III/IV disease, and the 5-year survival rate is a dismal 30%.
18 Mortality for this disease has not markedly changed since the 1930s² and this is
19 because ovarian cancer cannot be detected at low stage by current screening
20 programs. Resolving this dilemma will require effective tools and methods to interrupt
21 the carcinogenic sequence at a point that permits either cure or prevention of tumor-
22 specific mortality.
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24 There is cogent clinical and molecular evidence to suggest that many if not all
25 cases of HGSCs arise from the fallopian tube. From the clinical end, it has been known
26 that reducing risk of BRCA1 and BRCA2 patients required removing the fallopian tube in
27 addition to the ovary³. Molecular analyses have shown that HGSC has gene
28 expression profiles more akin to those of fallopian tube epithelium than to ovarian
29 surface epithelium⁴. Finally, and most significantly, the pathological examination of risk
30 reduction salpingo-oophorectomies for germ-line BRCA1 and BRCA2 mutations has
31 uncovered pre-metastatic stages of HGSC (serous tubal intraepithelial carcinoma or
32 STIC) as well as premalignant tubal intraepithelial neoplasia (or serous tubal
33 intraepithelial lesions) ^{5,6}. In the fallopian tube model, STIC is considered the earliest
34 morphologic manifestation of serous carcinoma. STICs are composed of “secretory
35 cells,” the non-ciliated population of the endosalpinx. These cells, when neoplastic,
36 exhibit features including variable stratification, increased proliferation and loss of
37 nuclear polarity⁷.
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3 Most STICs are marked by mutant p53, same as their metastatic form, high-
4 grade serous cancer. Further analyses of BRCA1/BRCA2 mutation-associated fallopian
5 tubes have revealed the presence as well of a “latent precancer” - the “p53 signature”,
6 which has mutant p53 overexpression but retains cell polarity and lacks excessive cell
7 proliferation. Interestingly, p53 signatures have been found adjacent to STICs and in
8 several revealing examples have been shown to share the same p53 mutation as
9 HGSC suggesting a lineage relationship⁸. These compelling results demonstrate that
10 the fallopian tube is a site of origin of HGSC, the development of which follows the
11 classic multi-step carcinogenesis model. Importantly, latent precancers are common in
12 tubes of women who are not at genetic risk and between 40-60% of the serous cancers
13 in BRCA mutation-negative women also co-exist with STIC^{7 8} with a genetic link
14 between the two^{9 10}. Thus, STIC represents the earliest phase of most pelvic serous
15 cancers and targeted treatment or prevention of STIC is a valid goal in cancer
16 prevention. In parallel with the serous carcinogenic sequence is the one characterized
17 by putative stem cell outgrowths or SCOUTs. These proliferations lack p53 mutations
18 but share many attributes with intraepithelial neoplasms, altered expression levels of
19 certain genes, including ALDH1, PAX2, EZH2, LEF1 and others. The impression from
20 these collective entities is that the tube is prone to both self-limited and potentially
21 malignant intraepithelial proliferations.
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24 HGSCs presumably arise from non-ciliated cells of the fallopian tube (secretory cells)
25 but the precise relationship between these cells and stem cells in the tube is not
26 understood, in part because of a lack of detailed *in vitro* studies of putative stem cells.
27 Herein, we report a fallopian tube stem cell model based on a cell culture paradigm of
28 both limited (immortalization) and aggressive (transformation) cell outgrowth. This
29 model is superimposed on a similar *in vivo* paradigm of proliferative lesions seen in the
30 fallopian tube. The goal of this exercise is to not only divine molecular perturbations
31 marking the transition from STIC to metastatic disease but also those that highlight the
32 loss of growth control in the early phases of neoplasia.
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35 **Methods**

36 Case material

This study was approved by the Brigham and Women's Human Investigation Committee and involved the use of discarded fresh and archived tissues. Case material for gene expression analysis and histology consisted of the following epithelia/lesions: (1) normal oviduct and HGSC paired samples (n = 10) and (2) normal oviduct, STIC and invasive HGSC lesions from each patient section (n = 6). Cases for immunohistochemistry were selected by one of us (CPC) using criteria that have been previously described¹⁰.

Stem cell culture and differentiation

Fallopian tube tissue was obtained from discarded surgical specimens of women undergoing benign procedures. Discarded fetal fallopian tube tissues were obtained under an approved IRB protocol. Disaggregated cells were cultivated onto a feeder layer of lethally irradiated 3 T3-J2 cells in stem cell culturing media (SCM-6F8)¹¹. Clonal analysis and *in vitro* ALI differentiation were based on previously described methods for lung epithelial stem cells¹².

Xenografts of transformed FTSCs

Fallopian tube stem cells were infected with retroviruses expressing c-Myc, hTERT, and SV40 large T antigen (SV40 large T and hTERT for immortalization, and SV40 large T, hTERT and c-Myc for transformation). In brief, 200,000 stem cells were plated onto a lawn of feeder cells in 3cm culture dishes and transduced three days later. After 48hr, cells were split 1:5 onto new lawns and grown and passaged for four weeks before plating onto culture plates without feeder cells for an additional four weeks. Individual colonies were selected and tested for growth in soft agar, and positive colonies selected for expansion and transplantation. Two thousand transformed cells (expressing SV40 large T antigen, hTERT and c-myc) were injected subcutaneously into six-week-old female NSG (NOD.Cg-*Prkdc*^{scid}/*Il2rg*^{tm1Wjl}/SzJ) mice following the protocols approved by BRC IACUC #110643 at the Agency for Science Technology and Research (A*STAR) Singapore. Visible tumors appeared typically at two weeks and were harvested following euthanasia and analyzed by histology and expression microarray.

Histology and immunofluorescence

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3 Histology, immunohistochemistry (IHC), and immunofluorescence (IF) were performed
4 following standard lab protocols. For IF and IHC staining, 4% paraformaldehyde-fixed
5 slides were subjected to antigen retrieval in citrate buffer (pH 6.0, Sigma-Aldrich, USA)
6 at 120 °C for 20 min, and blocking procedure was performed with 5 % bovine serum
7 albumin (BSA, Sigma-Aldrich, USA) and 0.05 % Triton X-100 (Sigma-Aldrich, USA) in
8 DPBS(-) (Gibco, USA) at room temperature for 1 hr. Cells cultured on 3T3 and air-liquid
9 interface culture were fixed with 4% formaldehyde at 4°C overnight and directly used in
10 staining. All primary antibodies used in this study and staining condition were
11 summarized in Supplemental Table 1. For IHC, detection was completed with the
12 Vectastain ABC kit (Cat No PK-6102; Vector Laboratories, Inc, Burlingame, CA, USA)
13 with a liquid DAB-plus substrate kit (Cat No 00-2020). Slides were counterstained with
14 Hematoxylin Stain 3 (Cat No CS402-1D). Stained slides were stored at 4 °C in the dark
15 and all images for section slides were captured by using the Inverted Eclipse Ti-Series
16 (Nikon, Japan) microscope with Lumencor SOLA light engine and Andor Technology
17 Clara Interline CCD camera and NIS-Elements Advanced Research v.4.13 software
18 (Nikon, Japan) or LSM 780 confocal microscope (Carl Zeiss, Germany) with LSM
19 software. Bright field cell culture images were obtained on an Eclipse TS100
20 microscope (Nikon, Japan) with Digital Sight DSFi1camera (Nikon, Japan) and NIS-
21 Elements F3.0 software (Nikon, Japan).
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39 Laser captured microdissection

40 Fresh surgical specimens from 10 independent women for normal oviduct and HGSC
41 and 6 independent women for normal, STIC and invasive STIC were embedded in OCT,
42 sectioned on a cryostat, and stained with hematoxylin to morphologically identify each
43 region. Twelve serial frozen sections of each tissue sample were microdissected using
44 a PALM microbeam instrument (Carl Zeiss, Germany), and each selected cell
45 population from different slides of the same patient were pooled. Total RNAs were
46 extracted using the Pico Pure RNA extraction kit (Life technologies, USA).
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55 Microarray

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3 For normal fallopian tube epithelium and paired HGSC samples from 10 patients and
4 FTSC (stem cells, immortalized, transformed and xenograft) samples, total RNA
5 processing and hybridization were performed on Affymetrix human U133 plus 2.0 Array
6 chips (Affymetrix, CA, USA). For normal fallopian tube epithelium, STIC and invasive
7 STIC from 6 patients, total RNAs were amplified using the WT Pico RNA Amplification
8 System V2 and Encore Biotin Module (NuGEN Technologies, USA). Amplified DNA
9 samples were prepared according to manufacturer's instructions and hybridized onto
10 GeneChip Human Exon 1.0 ST Array (Affymetrix, CA, USA). GeneChip operating
11 software was used to process all the Cel files and calculate probe intensity values. To
12 validate sample quality, quality check was conducted using Affymetrix Expression
13 Console software. The intensity values were log2-transformed and imported into the
14 Partek Genomics Suite 6.6 (Partek Incorporated, MO, USA). For GeneChip Human
15 Exon 1.0 ST Array, exons were summarized to genes and a 1-way ANOVA was
16 performed to identify differentially expressed genes. P-values and fold-change numbers
17 were calculated for each analysis.
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Bioinformatics for gene expression

Unsupervised clustering and heatmap generation were performed with sorted datasets by Euclidean distance on average linkage clustering with selected probe sets by Partek Genomics Suite 6.6. Gene Set Enrichment Analysis (GSEA; Subramanian et al., 2005) was performed to compare 1) STIC with invasive STIC, and 2) immortalized FTSC and FTSC, respectively. To find enriched pathways, DAVID bioinformatics resources (<http://david.abcc.ncifcrf.gov/>) were used¹³.

Accession numbers

Datasets generated for this study have been submitted to the National Center for Biotechnology Information Gene Expression Omnibus (GEO) database under GSE69428 for normal oviduct and HGSC from 10 patients, GSE69453 for FTSC-ALI, and transformed FTSCs (stem cell, immortalized, transformed and xenografts) and GSE69429 for normal fallopian tubal epithelium, STIC and invasive STIC from 6 patients.

Results

Cloning, immortalizing and transforming the fallopian tube stem cells.

If the fallopian tube is the origin of serous cancer, one possible mechanism for the evolution of cancer is a dysregulation of indigenous stem cells. We therefore set out to clone the stem cells of the fallopian tube using methods to clone columnar epithelial stem cells such as human intestinal stem cells¹¹. Using this method, we were able to generate clones of fallopian tube stem cells that contain many small, undifferentiated and highly proliferative (Ki67+) cells that can propagate through multiple passages

(Figure 1a). These stem cell clones show strong and consistent staining with markers of fallopian tube epithelial cells (PAX8) (Figure 2a). In our recent work on cloning adult stem cells from human airway and human intestine^{11 12}, we established a pedigree analysis method to examine the multipotential differentiation ability from a single stem cell. The high clonogenic capacity of fallopian tube stem cells allowed us to use the same approach to rapidly generate single cell “pedigree” lines of expansion and characterization of their lineage fates upon induced differentiation in air-liquid interface (ALI) cultures. Following FTSC differentiation, we found through immune-staining with specific antibodies and RT-PCR with specific primers that one single fallopian tube stem cell (Foxj1-, acetylated tubulin-, TA73-, Sall2-, BCL2-, PAX2-) can give rise to both ciliated cells (Foxj1+, acetylated tubulin+, TA73+, Sall2+) and secretory cells (Foxj1-, acetylated tubulin-, BCL2+, PAX2+)¹⁴ (Figure 1b and c). Moreover, the same FTSC pedigree line can be induced to differentiate into squamous metaplasia (p63+/Krt5+) in 3D Matrigel assay¹⁵. We next compared the FTSCs and their differentiated structure in ALI by gene expression. FTSCs showed high expression of several known adult stem cell markers such as Lrig1¹⁶, Lgr6¹⁷ and regulators of self-renewal such as EZH2¹⁸ and FOXM1¹⁹, TCF4²⁰. Interestingly, we did not find high expression of Lgr5²¹ in FTSCs. While the differentiated cells lost the expression of stem cell markers, they showed significantly increased expression of genes associated with ciliated cell and secretory cell differentiation such as genes in the Dynein family²² and MUC13²³ (Figure 1d).

To examine whether the fallopian tube stem cells are the cell of origin of high-grade serous cancer, we introduced SV40/ hTERT or SV40/hTERT/c-MYC into these

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3 cells by retroviral infection to induce immortalization or transformation of these cells
4 (Figure 1e). We showed while both immortalized and transformed FTSCs gained the new
5 property of growing without the support of irradiated 3T3-J2 fibroblast feeder, the transformed
6 FTSCs lost contact inhibition and showed fibroblast like morphology in the petri dish (Figure 1f,
7 upper). Moreover, both immortalized and transformed FTSCs formed sphere structures in
8 growth-factor-reduced Matrigel in 5 days, but transformed FTSCs generated the irregular
9 structures around 10 times larger in comparison with small and round spheres derived from
10 immortalized FTSCs (Figure 1f, lower). A heat map of differentially expressed genes in whole-
11 genome transcriptome analysis of FTSCs, immortalized and transformed FTSCs showed
12 distinct expression profile differences between normal FTSCs and transformed FTSCs (Figure
13 1d and supplementary table 2). Interestingly, immortalized FTSCs expressed at the moderate
14 level many genes that are highly expressed in transformed FTSCs (Figure 1g). Gene ontology
15 Analysis was performed to identify the gene pathways significantly enriched in transformed
16 cells including DNA replication and DNA repair (Supplemental Figure 1a). In addition, a highly
17 amplified gene in ovarian cancer, c-MYC was used as the transforming agent²⁴. Consistently,
18 we observed that downstream genes of c-MYC are highly enriched in transformed FTSCs but
19 not in immortalized FTSCs (Supplemental Figure 1b).
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33 **Transformed fallopian tube stem cells gave rise to high-grade serous cancer.**

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38 In order to examine whether the transformed fallopian tube stem cells belong in the
39 serous carcinogenic pathway, we injected subcutaneously two thousand transformed fallopian
40 tube stem cells into the immunodeficient (NOD.Cg-Prkdc^{scid} Il2rg^{tm1Wjl}/SzJ) mice²⁵ and
41 observed the formation of palpable tumor in two weeks. The xenografted tumors demonstrate
42 all the pathological and immunological hallmarks of human high-grade serous cancer, such as
43 gain of p53, EZH2 and MUC4 expression
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46 (Figure 2a)^{15 26 27}. To understand whether FTSC^t xenograft tumors resemble human high-
47 grade serous cancer at the level of gene expression, we first compared RNA from ten
48 microdissected histologically normal fallopian tube epithelium and paired high-grade serous
49 cancer tumor samples on expression microarray chips. These data revealed a significant two-
50 or-more-fold alteration (P<0.5) of the expression in 2395 genes that is
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3 presented in a heatmap (Figure 2b and supplementary table 3). Of the 2395 genes,
4 1017 genes are up-regulated, and in contrast, 1378 genes are down regulated in tumor
5 samples. The further analysis showed that FTSC^t xenograft tumors, just like HGSC,
6 also expressed these HGSC related genes in a similar manner.
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9 To clarify the function of the genes that we identified in the study and uncover the
10 pathways that conceivably could be targeted to lead to tumor cell death for the therapeutic
11 purpose, we uncovered a number of druggable targets in HGSC such as Enhancer of Zeste
12 Homolog 2. (EZH2). EZH2 is a histone methyl transferase (HMT) and a member of the
13 polycomb group of genes (PcG) regulating (suppressing) transcription through nucleosome
14 modification, chromatin remodeling, and interaction with other transcription factors. Several
15 studies have demonstrated that EZH2 is involved in oncogenesis and consistently, high
16 EZH2 transcript and protein levels have been associated with aggressive tumor behavior,
17 chemo-resistant tumor stem-like side populations and overall poor clinical outcome in
18 ovarian, breast, prostate and bladder cancer patients²⁸. We showed that the protein
19 expression of EZH2 is upregulated in precancerous lesion of HSGC (p53 signature²⁹, STIC,
20 invasive serous cancer and FTSC^t xenograft tumors (Figure 2c). Consistent with the
21 increased expression of EZH2 in HGSC and xenograft tumor, the expression of downstream
22 targets of EZH2 was significantly down regulated compared with normal fallopian tube
23 epithelium (Figure 2d). Moreover, treating the transformed fallopian tube stem cells with
24 EZH2 inhibitor that specifically blocks EZH2 activity³⁰ led to dramatically decreased cell
25 proliferation based on the diminished Ki67 antibody staining and drastic decreased structure
26 size in the Matrigel (Figure 2e).
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29 **Resolving molecular alterations in STIC and its progression to invasive serous
30 cancer.**
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33 Although advanced serous cancer has been proposed to result from STIC
34 progression, there has not been transcriptome analysis to demonstrate the molecular
35 progression from STIC to advanced serous cancer. To better understand potential links
36 between these entities via markers of progression, we used the LCM approach to
37 isolate normal fallopian tube epithelium, STIC and advance serous cancer from the
38 same patient (Figure 3a). A heatmap of differentially expressed genes in these datasets
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3 showed distinct expression profile between normal fallopian tubal epithelium and
4 advanced serous cancer among six patients. In contrast, STIC showed significant
5 overlap with both normal epithelium and advanced cancer (Figure 3b). Gene Set
6 Enrichment Analysis (GSEA) was performed to identify the gene pathways significantly
7 enriched in both STIC and advanced cancer or uniquely changed in advanced serous
8 cancer. The pathways involved in cell proliferation, genomic instability and survival are
9 aberrantly expressed at the early stage of serous carcinogenesis and are followed by
10 deregulation of the pathways involved in angiogenesis and cell adhesion (Figure 3c).
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12 Furthermore, we particularly focused on the secreted proteins that are highly
13 expressed in STIC or invasive serous cancer with the goal to use them as biomarkers
14 for early detection of HGSC. We identified eight genes significantly upregulated in
15 invasive cancer and three of them are already upregulated in the localized tubal tumor
16 (STIC) (Figure 3d). Among them, SPP1 (osteopontin), SPARC (Osteonectin) and
17 VCAN (Versican) have been reported to be overexpressed in various human cancers.
18 Particularly, osteopontin levels in plasma were significantly higher in patients with
19 epithelial ovarian cancer compared with those of healthy controls and patients with
20 other gynecologic cancers³¹.
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33 Uncovering early molecular changes associated with STIC

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35 The data presented here support the existing hypothesis that the fallopian tube is
36 the site of origin of high-grade serous cancer and the STIC is the non-invasive, pre-
37 metastatic form of high-grade serous cancer. A heatmap including 62 genes (>2 folds,
38 p<0.05) was generated to show the genes that were aberrantly upregulated in common
39 between STIC and matched invasive cancer (Figure 4a and supplementary table 4).
40 Among these 62 genes, Pituitary tumor transforming gene (PTTG1) and Cyclin E1
41 (CCNE1) (Supplemental Figure 2a) are particularly interesting because they have been
42 implicated in early oncogenesis through their driving role in cellular transformation^{32 33}.
43 In order to validate some of these genes, we next performed the immunohistochemistry
44 using the specific antibodies for PTTG1 and CCNE1 on patient-matched sections of
45 normal fallopian tube epithelium, STIC and invasive cancer. While the protein
46 expression of these two markers is barely detectable in normal fallopian tube
47 epithelium, they are highly expressed in STIC and invasive cancer (Figure 4b).
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We next hypothesized that among aberrantly expressed genes in STIC, there is a group of genes expressing during cellular immortalization, which is the first step towards malignancy³⁴. In order to test this hypothesis, we compared upregulated genes in immortalized FTSCs and STIC and uncovered 123 genes (>2 folds, p<0.05) that overlap in these two entities (Figure 4c and supplementary table 5). Among them, genes such as Stathmin1, a microtubule destabilizing protein³⁵, Ect2, a Rho guanine nucleotide exchange factor³⁶, Forkhead Box M1 (FOXM1), a transcription factor regulating cell cycle³⁷ have been suggested playing critical roles in tumor initiation of HGSC (Figure 4d and supplementary Figure 2b).

Discussion

The perception of ovarian epithelial carcinogenesis is changing rapidly since the proposal of the hypothesis that many of these tumors appear to originate in the fallopian tube²⁹. In 2012, Gilbert and colleagues further supported this hypothesis. Among their patients with “early” HGSC 78% the cancer had originated from the fallopian tube, peritoneum, or both³⁸. Recently another report noted that in the general patient population, incidentally discovered non-uterine high-grade serous carcinomas arise in the fallopian tube in most cases: further evidence for the tubal origin of high-grade serous carcinomas³⁹.

In this study, we cloned stem cells from human fallopian tube and demonstrated that transformed fallopian tube stem cells can develop to aggressive HGSC in mouse xenograft models in a short time. The xenografted tumor shared all the hallmark features with HGSC, further supporting the fallopian tube as the site of origin of serous cancer (Figure 5). Attempts to culture oviductal epithelial cells have been made previously, including efforts to model HGSC^{14 40 41}. However this study is the first to show that stem cells of fallopian tube can be maintained in culture in their elemental state and using the pedigree approach, are capable of multipotent differentiation from one single stem cell in the fallopian tube. Importantly, this platform of culturing FTSCs faithfully and robustly *in vitro* provided us a unique opportunity of functionally studying putative oncogenes or tumor suppressors discovered in recent cancer genome analysis through genetic editing of patient-derived FTSCs. Moreover, in this study we found that

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3 several putative oncogenes were significantly overexpressed at the step of FTSC
4 immortalization prior to the occurrence of transformation. Among them, Stathmin 1 has
5 been proposed as a marker expressed in early pelvic serous carcinomas³⁵; CXCR4 and
6 its ligand CXCL12 have been suggested as the key determinants of tumor initiation and
7 metastasis of ovarian cancer⁴²; Forkhead Box M1 (FOXM1) has been reported as a key
8 regulator of tumorigenesis by increasing proliferative activity and leading to uncontrolled
9 cell division³⁷. EZH2, a negative regulator of transcription was also upregulated two-fold
10 with immortalization. Interestingly, our previous study showed the PAX2-null progenitor
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18 cell growth (secretory cell outgrowth, SCOUTs) in the fallopian tube also expressed
19 strongly both EZH2 and Stathmin 1¹⁵. This correlation led us to propose the link
20 between FTSC immortalization and the development of early proliferations in the tube,
21 either SCOUTs or lower grade STINs. Based on these correlations it appears that these
22 gene perturbations associated with immortalization might occur prior to or even in the
23 absence of the serous cancer, in which case their value as predictors of malignancy
24 could be limited by their lack of specificity as actionable values. However, they could
25 conceivably be targeted as co-determinants of neoplastic progression with the goal of
26 depriving the serous carcinogenic sequence of a participating pathway.
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29 The stage at which an ovarian cancer is detected is the single most important
30 factor influencing outcome and interrupting ovarian cancer when it is curable will require
31 addressing early disease in the distal fallopian tube. Early molecular signatures that are
32 specific for these neoplasms are of paramount importance given their potential value in
33 detecting neoplasia via analysis of fluids in the lower genital tract⁴³. Given the fact that
34 many STICs do not have a HGSC outcome, we believe that there is a window of
35 opportunity where patients with potentially lethal precursors can be identified through
36 screening and spared a death from this malignancy.
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39 It would be hoped that a molecular analysis of early lesions might provide an
40 array of targets that are either secreted by these cells or presented on the cell surface
41 for screening and therapeutic value, respectively. Monoclonal antibodies to secreted
42 proteins have the potential to form the basis of population-wide screening methods from
43 blood or cervical fluid for those at risk who might benefit from salpingectomy.
44 Monoclonal antibodies to cell surface markers in these lesions might assist in alternative
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detection via imaging technologies as the technology evolves. An important question that must be addressed is whether the parallels between immortalized cells *in vitro* and proliferations *in vivo* signify a background of accrued biologic events that both precede - and are needed for - progression to malignancy. Thus the challenge will be to tease out those molecular events that are biologically significant and when intervened will prevent subsequent malignancy.

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This paper has not been previously published. Preliminary findings with clonogenic tubal epithelial cells have been previously described by Ning et al¹⁵. The authors have no conflicts of interest or relevant financial relationships. This study was approved by the Brigham and Women's Hospital Institutional Review Board. Array data is displayed in Supplemental Figure 2.

Abbreviations

STIC - serous tubal intraepithelial carcinoma; FTSC - fallopian tube stem cells;
HGSC – high grade serous cancer; ALI – air-liquid interface culture

Contribution of the coauthors are as follows:

Author	Design	Data collection	Data analysis	Data Interpretation	Literature search	Figures	Manuscript writing

1	Yamamoto	X	X	X	X	X		X
2	Ning	X	X	X	X			
3	Howitt		X	X	X			
4	Mehra		X	X	X			
5	Wu		X	X	X			
6	Wang		X	X	X			
7	Hong		X	X	X			
8	Tay		X	X	X			
9	Zhang		X	X	X			
10	Kern		X	X	X			
11	Nagarajan			X	X			
12	Choolani	X		X	X	X		X
13	Torti			X	X			X
14	Brewer			X	X			X
15	McKeon	X		X	X	X	X	X
16	Crum	X		X	X	X	X	X
17	Xian	X	X	X	X	X	X	X

Illustrations

Figure 1. Cloning, immortalization and transformation of the fallopian tube stem cells. a. Cloned FTSC marked with proliferation marker Ki67 (green) and occasional expression of ciliated marker FOXJ1 (red). b ALI differentiation culture of FTSC stained with FOXJ1 (red) and acetylated tubulin (green). c. RT-PCR of selected markers. d. Heatmap of selected genes from whole-genome transcriptome analysis. e. Schematic of FTSC immortalization and transformation *in vitro*. f. Morphological difference of FTSCⁱ and FTSC^t on plastic culture dishes and in 3D Matrigel assay. g. Progressive change of gene expression among FTSC, FTSCⁱ and FTSC^t (n = 2, each). Genes with increased expression (>1.5 fold and p < 0.05 in each, 654 genes) following transformation were selected for heatmap production.

Figure 2. FTSC^t xenograft tumor resembles human high-grade serous cancer. a. *Upper panel*, 2K FTSC^t cells (PAX8, red) were injected into NSG mice and palpable tumor was observed in two weeks. *Lower panel*, Xenograft tumor expressed HGSC hallmark genes MUC4, p53 and PAX8. b. A heatmap showing FTSC^t xenograft tumors and invasive SC

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3 shared similar gene expression profile (FTSC^t tumor: n = 3; invasive SC: n = 10 and
4 paired normal oviduct: n = 10; 2395 genes selected, > 2 folds and p < 0.05). c. EZH2
5 protein expressed in multiple stages of HGSC development including lower grade
6 serous tubal intraepithelial neoplasia and secretory cell outgrowths¹⁵. d. EZH2 target
7 genes were downregulated in FTSC^t xenograft tumors and invasive SC. e. Selective
8 inhibition of EZH2 by its inhibitor (3-Deazaneplanocin A) blocked FTSC^t cell proliferation
9 in a matrigel culture. Ki67 (red) stained for proliferating cells. Dapi (blue) stained nuclei.
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17 Figure 3. Molecular correlates of progression from STIC to invasive cancer. a. *Left*,
18 Histology of the sections used for Laser captured microdissection (LCM) of normal
19 fallopian tube epithelium, STIC and invasive cancer; *Right*, p53 antibody staining
20 showing prominent expression of p53 protein in STIC and invasive cancer. b. Six
21 heatmaps showing the progressive gene expression from STIC to invasive cancer in
22 individual patients (genes differentially expressed in invasive cancer compared with
23 normal FT epithelium were selected, >2 folds and p<0.05). c. Gene set enrichment
24 analysis (GSEA) of invasive cancer vs. STIC highlighting angiogenesis and regulation of
25 cell adhesion in invasive cancer. d. Dot plots of selected genes highly expressed in
26 STIC and invasive cancer (normal fallopian tube: n = 6; STIC: n = 6; invasive SC: n = 6).
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37 Figure 4. Early molecular changes associated with FTSC immortalization and STIC. a.
38 A heatmap showing 62 genes (>2 folds, p<0.05) commonly overexpressed between
39 STIC and matched invasive serous cancer. b. Representative images of CCNE1 and
40 PTTG1 immunostaining on normal FT epithelium, STIC and invasive serous cancer. c.
41 Venn diagram of genes overexpressed in STIC (>1.5 fold, p<0.05) and immortalized
42 FTSC (>2 fold, p < 0.05). 123 genes were overlapped. d. Selected overlapping genes
43 and fold change.
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51 Figure 5. *In vitro* and *in vivo* correlations proposing a model of multi-step development
52 of HGSC originated from fallopian tube stem cells.
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3 Supplementary Figure 1. a. Pathways enriched in immortalized and transformed FTSCs
4 compared with normal FTSC ($p < 0.05$) are listed in the table. b. GSEA showed
5 enrichment of MYC target genes in transformed but not immortalized FTSC.
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11 Supplementary figure 2. a. Dot plots of PTTG1 and CCNE1 expression in normal
12 fallopian tube epithelium, STIC and invasive SC. b. Pathway analysis showed
13 significantly enriched pathways ($p < 0.05$) in immortalized FTSCs and STIC.
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Figure 1

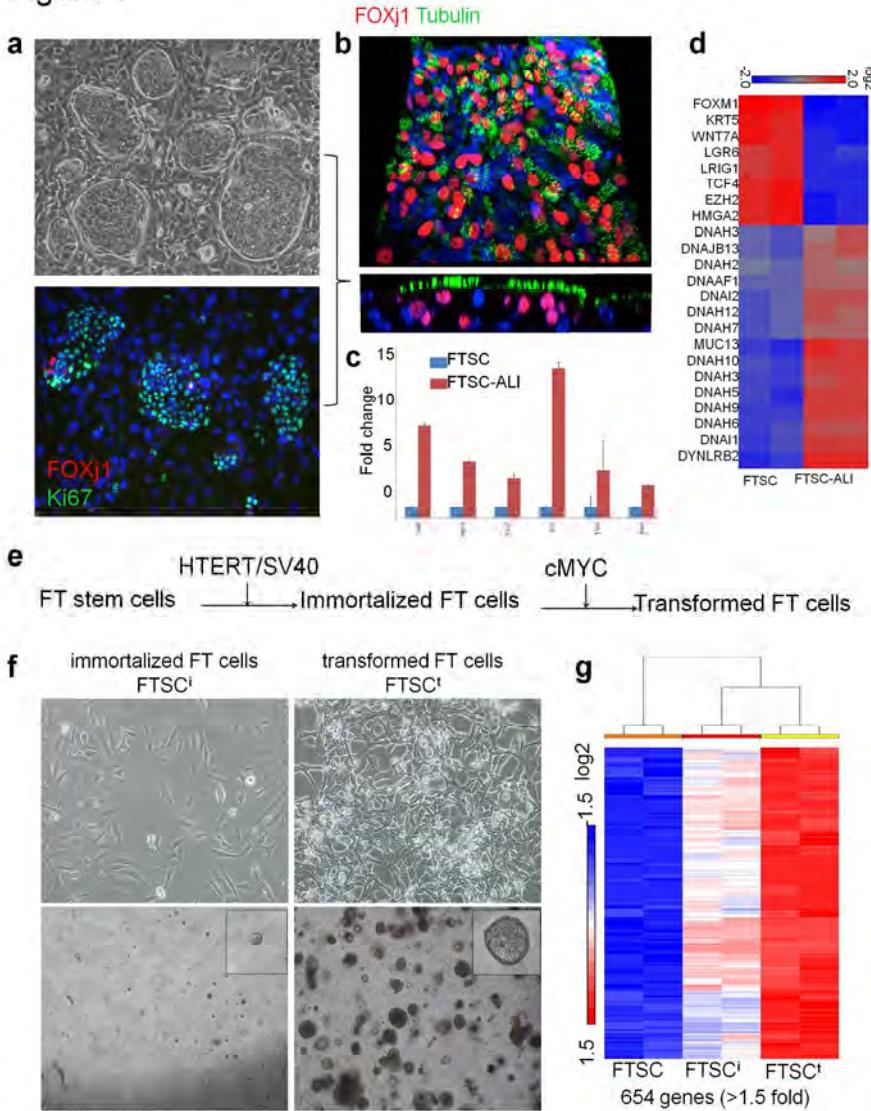


Figure 1. Cloning, immortalization and transformation of the fallopian tube stem cells. a. Cloned FTSC marked with proliferation marker Ki67 (green) and occasional expression of ciliated marker FOXJ1 (red). b. ALI differentiation culture of FTSC stained with FOXJ1 (red) and acetylated tubulin (green). c. RT-PCR of selected markers. d. Heatmap of selected genes from whole-genome transcriptome analysis. e. Schematic of FTSC immortalization and transformation in vitro. f. Morphological difference of FTSCⁱ and FTSC^t on plastic culture dishes and in 3D Matrigel assay. g. Progressive change of gene expression among FTSC, FTSCⁱ and FTSC^t ($n = 2$, each). Genes with increased expression (>1.5 fold and $p < 0.05$ in each, 654 genes) following transformation were selected for heatmap production.

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Figure 2

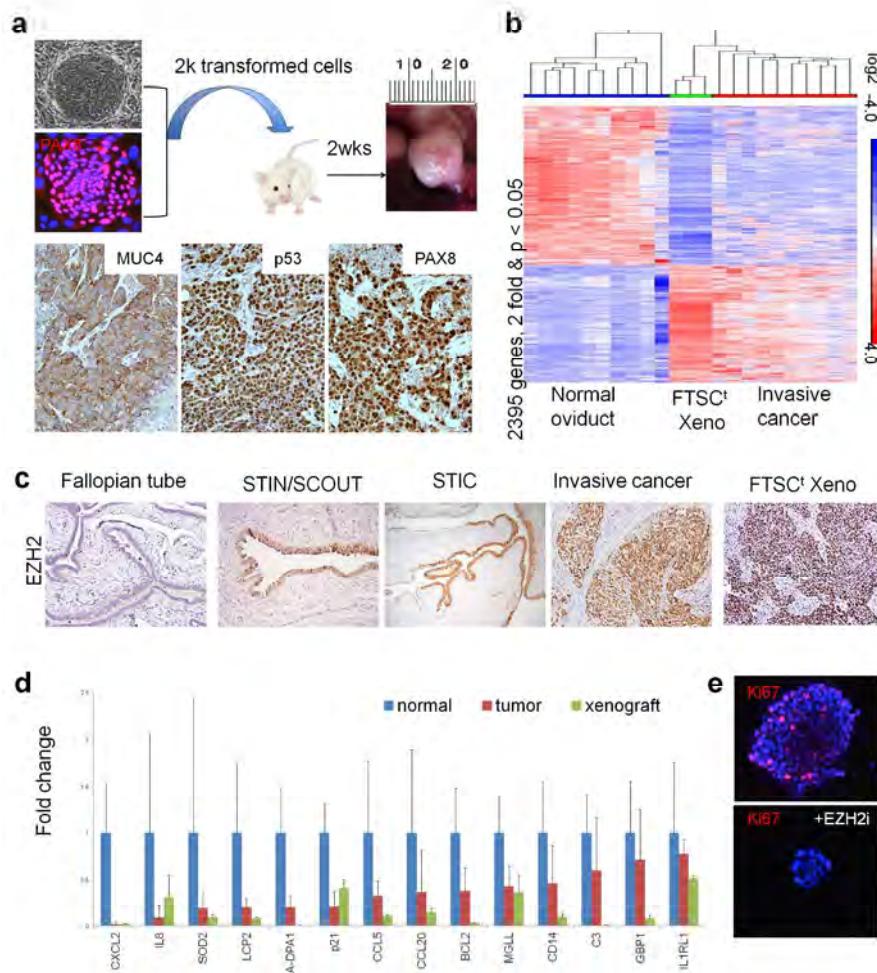


Figure 2. FTSCt xenograft tumor resembles human high-grade serous cancer. a. Upper panel, 2K FTSCt cells (PAX8, red) were injected into NSG mice and palpable tumor was observed in two weeks. Lower panel, Xenograft tumor expressed HGSC hallmark genes MUC4, p53 and PAX8. b. A heatmap showing FTSCt xenograft tumors and invasive SC shared similar gene expression profile (FTSCt tumor: $n = 3$; invasive SC: $n = 10$ and paired normal oviduct: $n = 10$; 2395 genes selected, > 2 folds and $p < 0.05$). c. EZH2 protein expressed in multiple stages of HGSC development including lower grade serous tubal intraepithelial neoplasia and secretory cell outgrowths¹⁵. d. EZH2 target genes were downregulated in FTSCt xenograft tumors and invasive SC. e. Selective inhibition of EZH2 by its inhibitor (3-Deazaneplanocin A) blocked FTSCt cell proliferation in a matrigel culture. Ki67 (red) stained for proliferating cells. Dapi (blue) stained nuclei.

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Figure 3

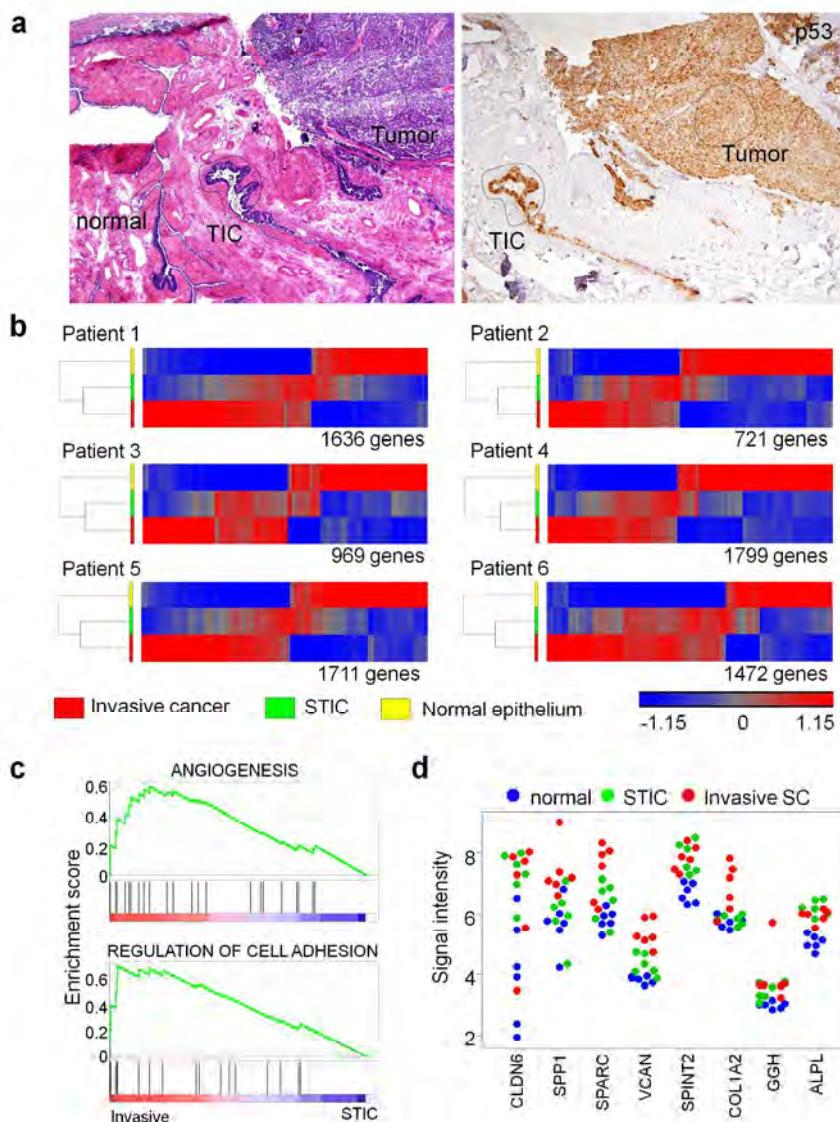


Figure 3. Molecular correlates of progression from STIC to invasive cancer. a. Left, Histology of the sections used for Laser captured microdissection (LCM) of normal fallopian tube epithelium, STIC and invasive cancer; Right, p53 antibody staining showing prominent expression of p53 protein in STIC and invasive cancer. b. Six heatmaps showing the progressive gene expression from STIC to invasive cancer in individual patients (genes differentially expressed in invasive cancer compared with normal FT epithelium were selected, >2 folds and $p < 0.05$). c. Gene set enrichment analysis (GSEA) of invasive cancer vs. STIC highlighting angiogenesis and regulation of cell adhesion in invasive cancer. d. Dot plots of selected genes highly expressed in STIC and invasive cancer (normal fallopian tube: $n = 6$; STIC: $n = 6$; invasive SC: $n = 6$).

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Figure 4

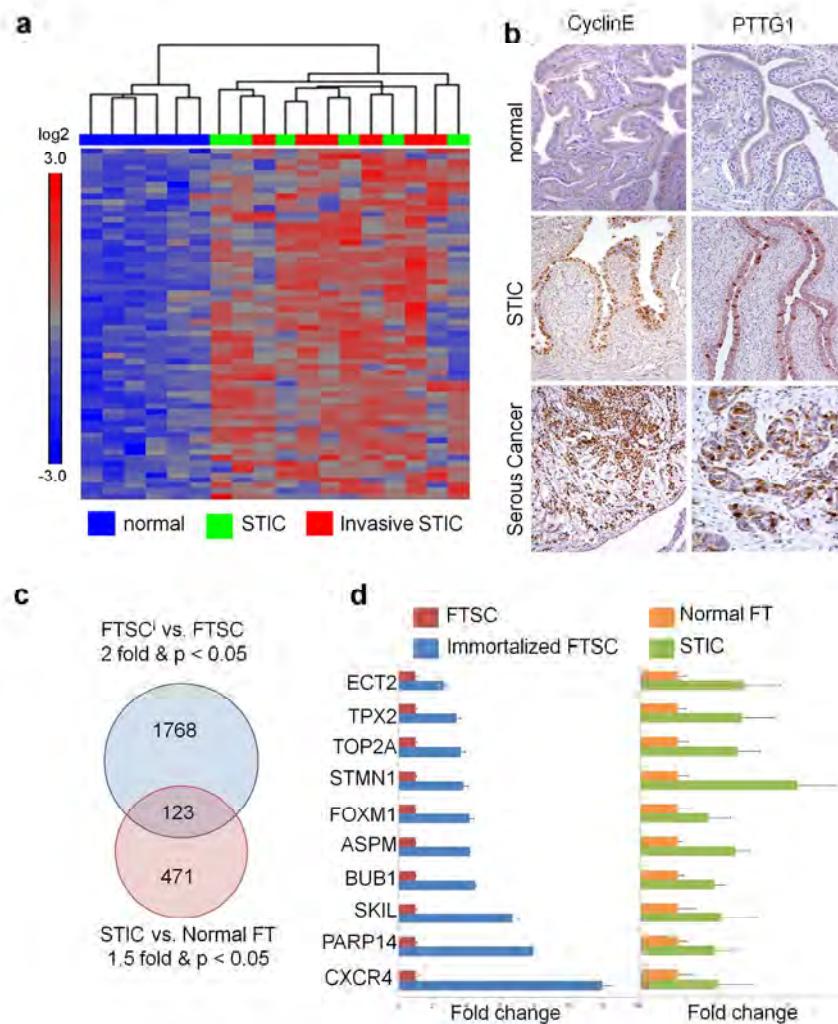


Figure 4. Figure 4. Early molecular changes associated with FTSC immortalization and STIC. a. A heatmap showing 62 genes (>2 folds, $p < 0.05$) commonly overexpressed between STIC and matched invasive serous cancer. b. Representative images of CCNE1 and PTTG1 immunostaining on normal FT epithelium, STIC and invasive serous cancer. c. Venn diagram of genes overexpressed in STIC (>1.5 fold, $p < 0.05$) and immortalized FTSC (>2 fold, $p < 0.05$). 123 genes were overlapped. d. Selected overlapping genes and fold change.

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Figure 5

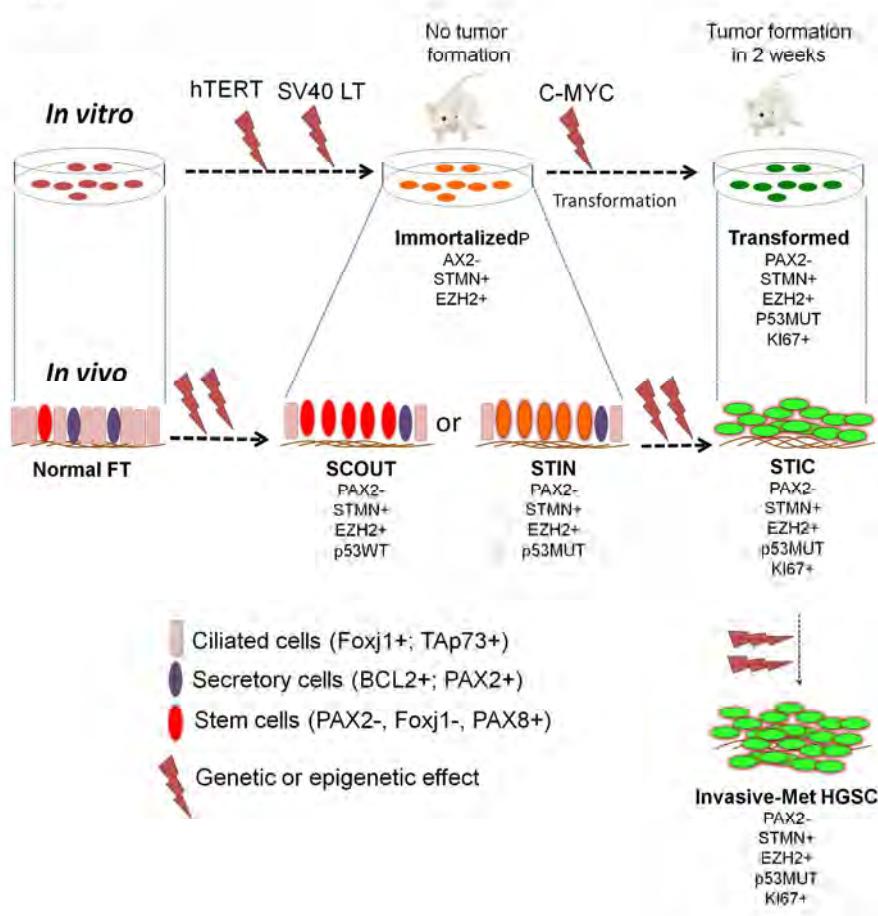


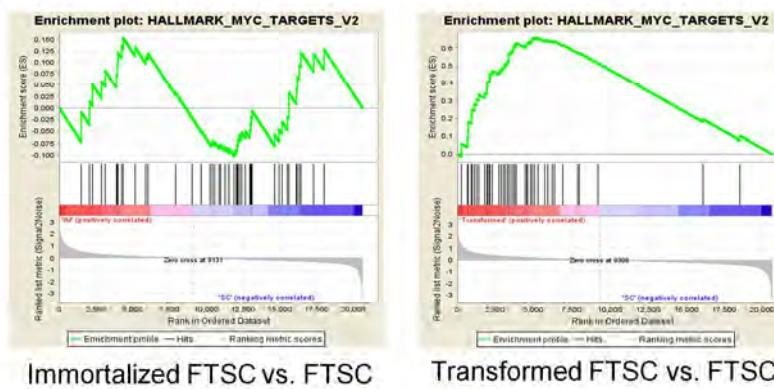
Figure 5. In vitro and in vivo correlations proposing a model of multi-step development of HGSC originated from fallopian tube stem cells.

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Supplemental Figure 1

a

Category	Count	PValue
DNA replication	10	1.52E-07
Cell cycle	14	1.13E-05
Aminoacyl-tRNA biosynthesis	8	5.70E-05
One carbon pool by folate	4	0.006716
Mismatch repair	4	0.018706
TGF-beta signaling pathway	7	0.020951
Nucleotide excision repair	5	0.023315
Glycine, serine and threonine metabolism	4	0.041123

b

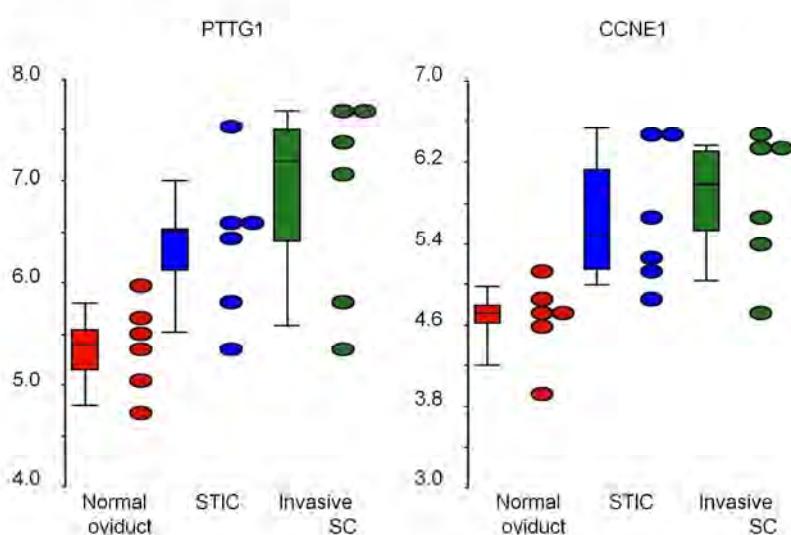
Immortalized FTSC vs. FTSC

Transformed FTSC vs. FTSC

Supplementary Figure 1. a. Pathways enriched in immortalized and transformed FTSCs compared with normal FTSC ($p < 0.05$) are listed in the table. b. GSEA showed enrichment of MYC target genes in transformed nut not immortalized FTSC.

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Supplemental Figure 2

a**b**

Term	%	PValue
Cell cycle	5.93	2.36E-05
Mismatch repair	2.54	0.005512
Progesterone-mediated oocyte maturation	3.39	0.008211
Oocyte meiosis	3.39	0.016025
Pathways in cancer	5.08	0.019728
p53 signaling pathway	2.54	0.04338

Supplementary Figure 2. a. Dot plots of PTTG1 and CCNE1 expression in normal fallopian tube epithelium, STIC and invasive SC. b. Pathway analysis showed significantly enriched pathways ($p < 0.05$) in immortalized FTSCs and STIC.
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Supplemental Table 1. Antibodies used

Antibody	Manufacturers	Cat. No.	Working Dilution
Alpha-Tubulin	Sigma-Aldrich	T9026	1:3000
CyclinE1	Abcam	ab3927	1:1600
EZH2	Leica Biosystems	NCL-L-EZH2	1:500
Foxj1	Sigma-Aldrich	HPA005714	1:500
MUC4	Invitrogen	18-2322	1:800
P53	Caibiochem	OP43	1:500
PAX8	Protein Tech	10336-1-AP	1:400
PTTG1	Sigma-Aldrich	HPA008890	1:1000

1 Supplementary Table 2 incrementally expressed:

5	Probeset ID	Gene Symbol
6	210587_at	INHBE
7	203548_s_at	LPL
8	1554242_a_at	COCH
9	235020_at	TAF4B
10	239352_at	SLC6A15
11	219295_s_at	PCOLCE2
12	226695_at	PRRX1
13	219911_s_at	SLCO4A1
14	240419_at	SLC6A15
15	214651_s_at	HOXA10-HOXA9 /// HOXA9
16	204394_at	SLC43A1
17	204794_at	DUSP2
18	206376_at	SLC6A15
19	203387_s_at	TBC1D4
20	219985_at	HS3ST3A1
21	210143_at	ANXA10
22	232263_at	SLC6A15
23	203386_at	TBC1D4
24	205885_s_at	ITGA4
25	223721_s_at	DNAJC12
26	1558404_at	LOC644242
27	207536_s_at	TNFRSF9
28	213113_s_at	SLC43A3
29	206261_at	ZNF239
30	236302_at	PPM1E
31	220615_s_at	FAR2
32	223722_at	DNAJC12
33	212813_at	JAM3
34	205884_at	ITGA4
35	206172_at	IL13RA2
36	238681_at	GDPD1
37	235343_at	VASH2
38	218976_at	DNAJC12
39	201578_at	PODXL
40	225516_at	SLC7A2
41	204521_at	FAM216A
42	235548_at	APCDD1L
43	1569582_at	LOC201651
44	207219_at	ZNF643
45	242931_at	LONRF3
46	1554918_a_at	ABCC4
47	218541_s_at	C8orf4
48	228956_at	UGT8

1	219969_at	TXLNG
2	200841_s_at	EPRS
3	210692_s_at	SLC43A3
4	232291_at	MIR17HG /// MIR18A /// M
5	238831_at	TMEM33
6	1554640_at	PALM2
7	213416_at	ITGA4
8	1555606_a_at	GDPD1
9	230763_at	SPATA17
10	226890_at	WDR35
11	236313_at	CDKN2B
12	205429_s_at	MPP6
13	218590_at	C10orf2
14	221648_s_at	AGMAT
15	222062_at	IL27RA
16	221586_s_at	E2F5
17	225285_at	BCAT1
18	229437_at	MIR155 /// MIR155HG
19	231984_at	MTAP
20	235644_at	CCDC138
21	238990_x_at	TRIM61
22	219262_at	SUV39H2
23	204956_at	MTAP
24	229596_at	AMDHD1
25	206085_s_at	CTH
26	225421_at	PM20D2
27	229715_at	B7H6
28	209406_at	BAG2
29	212816_s_at	CBS
30	236219_at	SLC35G1
31	209892_at	FUT4
32	208264_s_at	EIF3J
33	227892_at	PRKAA2
34	1553972_a_at	CBS
35	227607_at	STAMBPL1
36	236075_s_at	LOC100506676
37	202684_s_at	RNMT
38	212706_at	RASA4 /// RASA4B
39	214452_at	BCAT1
40	220251_at	DIEXF
41	228962_at	PDE4D
42	227896_at	BCCIP
43	219616_at	ACSS3
44	227932_at	ARIH2
45	242905_at	PNO1
46	235177_at	METTL21A
47	235733_at	GXYLT2

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2	202920_at	ANK2
3	220346_at	MTHFD2L
4	221088_s_at	PPP1R9A
5	243502_at	GJC1
6	228494_at	PPP1R9A
7	233737_s_at	LOC284561
8	242037_at	ASPH
9	212894_at	SUPV3L1
10	226517_at	BCAT1
11	238452_at	FCRLB
12	236917_at	LRRC34
13	1555882_at	SPIN3
14	212290_at	SLC7A1
15	218599_at	REC8
16	218936_s_at	CCDC59
17	217127_at	CTH
18	203163_at	KATNB1
19	207057_at	SLC16A7
20	229435_at	GLIS3
21	219731_at	CC2D2B
22	205047_s_at	ASNS
23	1559993_at	SFXN3
24	227916_x_at	EXOSC3
25	220370_s_at	USP36
26	222305_at	HK2
27	205541_s_at	GSPT2
28	212036_s_at	PNN
29	220698_at	MGC4294
30	205668_at	LY75
31	225100_at	FBXO45
32	230097_at	GART
33	204700_x_at	DIEXF
34	1552430_at	WDR17
35	224873_s_at	MRPS25
36	227606_s_at	STAMBPL1
37	233655_s_at	HAUS6
38	200790_at	ODC1
39	1555562_a_at	ZCCHC7
40	206613_s_at	TAF1A
41	1569183_a_at	CHM
42	228378_at	C12orf29
43	222624_s_at	ZNF639
44	201228_s_at	ARIH2
45	225142_at	JHDM1D
46	204491_at	PDE4D
47	1552625_a_at	TRNT1
48	235610_at	ALKBH8
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1	203622_s_at	PNO1
2	227856_at	C4orf32
3	226876_at	FAM101B
4	241866_at	SLC16A7
5	206204_at	GRB14
6	230258_at	GLIS3
7	223700_at	MND1
8	200975_at	PPT1
9	230166_at	KIAA1958
10	227037_at	PLD6
11	218591_s_at	NOL10
12	222736_s_at	TMEM38B
13	208541_x_at	TFAM
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46	213155_at	LOC339166 /// WSCD1
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21	228249_at	C11orf74
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1 genes (1.5 fold and p < 0.05) during progression (FTSC -> FTSCi -> FTSCt) 654 probes

2 4 Gene Title

5 inhibin, beta E

6 lipoprotein lipase

7 coagulation factor C homolog, cochlin (Limulus polyphemus)

8 TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105kDa

9 10 solute carrier family 6 (neutral amino acid transporter), member 15

11 12 procollagen C-endopeptidase enhancer 2

13 14 paired related homeobox 1

15 16 solute carrier organic anion transporter family, member 4A1

17 18 solute carrier family 6 (neutral amino acid transporter), member 15

19 20 HOXA10-HOXA9 readthrough /// homeobox A9 /// microRNA 196b

21 22 solute carrier family 43, member 1

23 24 dual specificity phosphatase 2

25 26 solute carrier family 6 (neutral amino acid transporter), member 15

27 28 TBC1 domain family, member 4

29 30 heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1

31 32 annexin A10

33 34 solute carrier family 6 (neutral amino acid transporter), member 15

35 36 TBC1 domain family, member 4

37 38 integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)

39 40 DnaJ (Hsp40) homolog, subfamily C, member 12

41 42 uncharacterized LOC644242

43 44 tumor necrosis factor receptor superfamily, member 9

45 46 solute carrier family 43, member 3

47 48 zinc finger protein 239

49 50 protein phosphatase, Mg²⁺/Mn²⁺ dependent, 1E

51 52 fatty acyl CoA reductase 2

53 54 DnaJ (Hsp40) homolog, subfamily C, member 12

55 56 junctional adhesion molecule 3

57 58 integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)

59 60 interleukin 13 receptor, alpha 2

61 62 glycerophosphodiester phosphodiesterase domain containing 1

63 64 vasohibin 2

65 66 DnaJ (Hsp40) homolog, subfamily C, member 12

67 68 podocalyxin-like

69 70 solute carrier family 7 (cationic amino acid transporter, y⁺ system), member 2

71 72 family with sequence similarity 216, member A

73 74 adenomatosis polyposis coli down-regulated 1-like

75 76 arylacetamide deacetylase (esterase) pseudogene

77 78 zinc finger protein 643

79 80 LON peptidase N-terminal domain and ring finger 3

81 82 ATP-binding cassette, sub-family C (CFTR/MRP), member 4

83 84 chromosome 8 open reading frame 4

85 86 UDP glycosyltransferase 8

1 taxilin gamma
2 glutamyl-prolyl-tRNA synthetase
3 solute carrier family 43, member 3
4 miR-17-92 cluster host gene (non-protein coding) /// microRNA 18a /// microRNA 19a ///
5 transmembrane protein 33
6 paralemmin 2
7 integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)
8 glycerophosphodiester phosphodiesterase domain containing 1
9 spermatogenesis associated 17
10 WD repeat domain 35
11 cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)
12 membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)
13 chromosome 10 open reading frame 2
14 agmatine ureohydrolase (agmatinase)
15 interleukin 27 receptor, alpha
16 E2F transcription factor 5, p130-binding
17 branched chain amino-acid transaminase 1, cytosolic
18 microRNA 155 /// MIR155 host gene (non-protein coding)
19 methylthioadenosine phosphorylase
20 coiled-coil domain containing 138
21 tripartite motif containing 61
22 suppressor of variegation 3-9 homolog 2 (Drosophila)
23 methylthioadenosine phosphorylase
24 amidohydrolase domain containing 1
25 cystathionase (cystathione gamma-lyase)
26 peptidase M20 domain containing 2
27 B7 homolog 6
28 BCL2-associated athanogene 2
29 cystathionine-beta-synthase
30 solute carrier family 35, member G1
31 fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)
32 eukaryotic translation initiation factor 3, subunit J
33 protein kinase, AMP-activated, alpha 2 catalytic subunit
34 cystathionine-beta-synthase
35 STAM binding protein-like 1
36 uncharacterized LOC100506676
37 RNA (guanine-7-) methyltransferase
38 RAS p21 protein activator 4 /// RAS p21 protein activator 4B
39 branched chain amino-acid transaminase 1, cytosolic
40 digestive organ expansion factor homolog (zebrafish)
41 phosphodiesterase 4D, cAMP-specific
42 BRCA2 and CDKN1A interacting protein
43 acyl-CoA synthetase short-chain family member 3
44 ariadne homolog 2 (Drosophila)
45 partner of NOB1 homolog (S. cerevisiae)
46 methyltransferase like 21A
47 glucoside xylosyltransferase 2

1 ankyrin 2, neuronal
2 methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like
3 protein phosphatase 1, regulatory subunit 9A
4 gap junction protein, gamma 1, 45kDa
5 protein phosphatase 1, regulatory subunit 9A
6 uncharacterized LOC284561
7 aspartate beta-hydroxylase
8 suppressor of var1, 3-like 1 (*S. cerevisiae*)
9 branched chain amino-acid transaminase 1, cytosolic
10 Fc receptor-like B
11 leucine rich repeat containing 34
12 spindlin family, member 3
13 solute carrier family 7 (cationic amino acid transporter, y+ system), member 1
14 REC8 homolog (yeast)
15 coiled-coil domain containing 59
16 cystathionase (cystathionine gamma-lyase)
17 katanin p80 (WD repeat containing) subunit B 1
18 solute carrier family 16, member 7 (monocarboxylic acid transporter 2)
19 GLIS family zinc finger 3
20 Coiled-coil and C2 domain containing 2B
21 asparagine synthetase (glutamine-hydrolyzing)
22 Sideroflexin 3
23 exosome component 3
24 ubiquitin specific peptidase 36
25 hexokinase 2
26 G1 to S phase transition 2
27 pinin, desmosome associated protein
28 uncharacterized MGC4294
29 lymphocyte antigen 75
30 F-box protein 45
31 phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phos-
32 digestive organ expansion factor homolog (zebrafish)
33 WD repeat domain 17
34 mitochondrial ribosomal protein S25
35 STAM binding protein-like 1
36 HAUS augmin-like complex, subunit 6
37 ornithine decarboxylase 1
38 zinc finger, CCHC domain containing 7
39 TATA box binding protein (TBP)-associated factor, RNA polymerase I, A, 48kDa
40 choroideremia (Rab escort protein 1)
41 chromosome 12 open reading frame 29
42 zinc finger protein 639
43 ariadne homolog 2 (*Drosophila*)
44 jumonji C domain containing histone demethylase 1 homolog D (*S. cerevisiae*)
45 phosphodiesterase 4D, cAMP-specific
46 tRNA nucleotidyl transferase, CCA-adding, 1
47 alkB, alkylation repair homolog 8 (*E. coli*)

1 partner of NOB1 homolog (S. cerevisiae)
2 chromosome 4 open reading frame 32
3 family with sequence similarity 101, member B
4 solute carrier family 16, member 7 (monocarboxylic acid transporter 2)
5 growth factor receptor-bound protein 14
6 GLIS family zinc finger 3
7 meiotic nuclear divisions 1 homolog (S. cerevisiae)
8 palmitoyl-protein thioesterase 1
9 KIAA1958
10 phospholipase D family, member 6
11 nucleolar protein 10
12 transmembrane protein 38B
13 transcription factor A, mitochondrial
14 anaphase promoting complex subunit 1 /// anaphase-promoting complex subunit 1-like ///
15 exonuclease 1
16 PMS1 postmeiotic segregation increased 1 (S. cerevisiae)
17 rabaptin, RAB GTPase binding effector protein 1
18 protein phosphatase 1, regulatory subunit 9A
19 transcription factor A, mitochondrial
20 F-box protein 45
21 GA binding protein transcription factor, alpha subunit 60kDa
22 SCO cytochrome oxidase deficient homolog 1 (yeast)
23 molybdenum cofactor sulfurase
24 methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like
25 primase, DNA, polypeptide 1 (49kDa)
26 phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phos
27 minichromosome maintenance complex component 10
28 SET domain containing 6
29 butyrophilin-like 9
30 zinc finger protein 638
31 minichromosome maintenance complex component 10
32 EP300 interacting inhibitor of differentiation 3
33 zinc finger, BED-type containing 3
34 general transcription factor IIH, polypeptide 2, 44kDa /// general transcription factor
35 5-methyltetrahydrofolate-homocysteine methyltransferase reductase
36 general transcription factor IIH, polypeptide 2, 44kDa
37 G protein-coupled receptor 107
38 tetratricopeptide repeat domain 26
39 protein kinase, AMP-activated, alpha 2 catalytic subunit
40 family with sequence similarity 101, member B
41 junction mediating and regulatory protein, p53 cofactor
42 POU class 2 homeobox 2
43 ankylosis, progressive homolog (mouse)
44 fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)
45 chromosome 20 open reading frame 112
46 homeobox A7
47 BRO1 domain and CAAX motif containing

1 ankyrin repeat domain 7
2 solute carrier family 25 (mitochondrial folate carrier) , member 32
3 bone morphogenetic protein receptor, type IB
4 tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)
5 BCL2-associated transcription factor 1
6 exosome component 2
7 replication factor C (activator 1) 3, 38kDa
8 HRAS-like suppressor
9 uncharacterized LOC100506392
10 zinc finger, BED-type containing 3
11 branched chain amino-acid transaminase 1, cytosolic
12 POU class 2 homeobox 2
13 glucoside xylosyltransferase 2
14 POU class 2 homeobox 2
15 solute carrier family 25 (mitochondrial iron transporter), member 37
16 chromosome 6 open reading frame 228
17 dedicator of cytokinesis 11
18 TMEM161B antisense RNA 1 (non-protein coding)
19 WAS protein family, member 3
20 ZNF790 antisense RNA 1 (non-protein coding)
21 MyoD family inhibitor domain containing
22 Uncharacterized LOC148189
23 uncharacterized LOC378805
24 Vpr (HIV-1) binding protein
25 hairy and enhancer of split 6 (Drosophila)
26 Rho GTPase activating protein 42
27 LON peptidase N-terminal domain and ring finger 2
28 HAUS augmin-like complex, subunit 7 /// three prime repair exonuclease 2
29 bone morphogenetic protein receptor, type IB
30 general transcription factor IIH, polypeptide 2B (pseudogene)
31 nuclear factor of kappa light polypeptide gene enhancer in B-cells 1
32 transcription factor A, mitochondrial
33 deleted in liver cancer 1
34 chromosome 17 open reading frame 58
35 cyclin-dependent kinase inhibitor 2A
36 Abelson helper integration site 1
37 homeobox A7
38 LON peptidase N-terminal domain and ring finger 2
39 low density lipoprotein receptor-related protein 8, apolipoprotein e receptor
40 nicotinamide phosphoribosyltransferase
41 microcephalin 1
42 solute carrier family 16, member 6 (monocarboxylic acid transporter 7)
43 laminin, alpha 4
44 KIAA1984
45 arylacetamide deacetylase (esterase)
46 GrpE-like 2, mitochondrial (E. coli)
47 tumor necrosis factor, alpha-induced protein 2

1 carbohydrate (chondroitin 4) sulfotransferase 11
2 phosphoserine aminotransferase 1
3 solute carrier family 25 (mitochondrial iron transporter), member 37
4 transcription factor A, mitochondrial
5 long intergenic non-protein coding RNA 338 /// small Cajal body-specific RNA 16
6 polymerase (DNA directed), epsilon 2, accessory subunit
7 activin A receptor, type IIA
8 T-complex-associated-testis-expressed 3
9 feline leukemia virus subgroup C cellular receptor 1
10 SFT2 domain containing 3 /// WD repeat domain 33
11 asparagine-linked glycosylation 10, alpha-1,2-glucosyltransferase homolog B (yeast)
12 uncharacterized LOC100507619
13 solute carrier family 25 (mitochondrial iron transporter), member 37
14 intercellular adhesion molecule 1
15 chromosome 14 open reading frame 149
16 ubiquitin protein ligase E3A
17 thioredoxin-like 4B
18 asparagine-linked glycosylation 10, alpha-1,2-glucosyltransferase homolog (S. pombe)
19 uncharacterized LOC100129518 /// superoxide dismutase 2, mitochondrial
20 UHRF1 binding protein 1
21 minichromosome maintenance complex component 7
22 defective in sister chromatid cohesion 1 homolog (S. cerevisiae)
23 dipeptidyl-peptidase 4
24 p21 protein (Cdc42/Rac)-activated kinase 2
25 spastic ataxia of Charlevoix-Saguenay (sacsin)
26 consortin, connexin sorting protein
27 cyclin-dependent kinase inhibitor 2A
28 3-oxoacid CoA transferase 1
29 seryl-tRNA synthetase
30 GA binding protein transcription factor, beta subunit 1
31 chromosome 6 open reading frame 228
32 EF-hand calcium binding domain 4B
33 digestive organ expansion factor homolog (zebrafish)
34 potassium channel tetramerisation domain containing 16
35 G patch domain and ankyrin repeats 1
36 zinc finger protein 202
37 solute carrier family 16, member 7 (monocarboxylic acid transporter 2)
38 ribosomal protein L23a pseudogene 7 /// ribosomal protein L23a pseudogene 82
39 low density lipoprotein receptor-related protein 8, apolipoprotein e receptor
40 zinc finger protein 26-like /// zinc finger protein 26
41 anaphase promoting complex subunit 1 pseudogene
42 uncharacterized LOC100509445 /// ovostatin homolog 2-like /// ovostatin 2
43 small nuclear ribonucleoprotein polypeptide A'
44 inositol 1,4,5-trisphosphate receptor interacting protein-like 2
45 zinc finger protein 566
46 suppressor of Ty 16 homolog (S. cerevisiae)
47 tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)

1 Fanconi anemia, complementation group B
2 RNA binding motif protein 15
3 transmembrane protein 133
4 retinoblastoma-like 1 (p107)
5 malic enzyme 1, NADP(+) -dependent, cytosolic
6 inositol 1,4,5-trisphosphate receptor interacting protein-like 2
7 structure specific recognition protein 1
8 digestive organ expansion factor homolog (zebrafish)
9 carbohydrate (chondroitin 4) sulfotransferase 11
10 ChaC, cation transport regulator homolog 2 (E. coli)
11 uncharacterized LOC100506290 /// uncharacterized LOC100653153 /// methyltransferase lik
12 long intergenic non-protein coding RNA 115
13 transducin (beta)-like 1X-linked
14 DEAH (Asp-Glu-Ala-His) box polypeptide 35
15 uncharacterized protein ENSP00000244321
16 minichromosome maintenance complex component 7
17 ankyrin repeat domain 10
18 coiled-coil domain containing 90A
19 solute carrier family 25 (pyrimidine nucleotide carrier), member 33
20 thioredoxin-related transmembrane protein 3
21 jumonji C domain containing histone demethylase 1 homolog D (S. cerevisiae)
22 solute carrier family 39 (zinc transporter), member 14
23 protein inhibitor of activated STAT, 2
24 replication factor C (activator 1) 3, 38kDa
25 ATPase type 13A3
26 suppressor of variegation 3-9 homolog 2 (Drosophila)
27 uncharacterized LOC100506090
28 phenylalanyl-tRNA synthetase, beta subunit
29 general transcription factor IIH, polypeptide 1, 62kDa
30 GABPB1 antisense RNA 1 (non-protein coding)
31 N-acetylglutamate synthase
32 ADAM metallopeptidase with thrombospondin type 1 motif, 3
33 SRR1 domain containing
34 rabaptin, RAB GTPase binding effector protein 1
35 ATPase, class VI, type 11C
36 uncharacterized LOC646762
37 polymerase (RNA) III (DNA directed) polypeptide K, 12.3 kDa
38 uncharacterized LOC100506922
39 TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 100kDa
40 cysteinyl-tRNA synthetase
41 consortin, connexin sorting protein
42 fatty acid binding protein 5 (psoriasis-associated)
43 interleukin enhancer binding factor 3, 90kDa
44 centrosomal protein 128kDa
45 FK506 binding protein 11, 19 kDa
46 cell division cycle 25 homolog A (S. pombe)
47 thymopoietin
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1 Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase
2 CREB/ATF bZIP transcription factor
3 UbiA prenyltransferase domain containing 1
4 FIP1 like 1 (*S. cerevisiae*)
5 TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 100kDa
6 helicase, lymphoid-specific
7 SDE2 telomere maintenance homolog (*S. pombe*)
8 NADH dehydrogenase (ubiquinone) complex I, assembly factor 4
9 IKAROS family zinc finger 5 (Pegasus)
10 tubulin, delta 1
11 general transcription factor IIH, polypeptide 1, 62kDa
12 helicase, lymphoid-specific
13 peptidylprolyl isomerase F
14 uncharacterized LOC100505549
15 activin A receptor, type IIB
16 ZEB1 antisense RNA 1 (non-protein coding)
17 cleavage and polyadenylation specific factor 6, 68kDa
18 nucleoporin 107kDa
19 TATA box binding protein (TBP)-associated factor, RNA polymerase I, B, 63kDa
20 chromosome 1 open reading frame 43
21 importin 11
22 zinc finger, AN1-type domain 4
23 U2 snRNP-associated SURP domain containing
24 U2 snRNP-associated SURP domain containing
25 centrosome and spindle pole associated protein 1
26 cysteinyl-tRNA synthetase
27 periphilin 1
28 HEN1 methyltransferase homolog 1 (*Arabidopsis*)
29 cyclin J
30 tubulin, delta 1
31 nucleoporin 35kDa
32 DNA cross-link repair 1A
33 chromosome 9 open reading frame 72
34 dual specificity phosphatase 5
35 solute carrier family 25 (mitochondrial iron transporter), member 37
36 DDHD domain containing 1
37 serine/arginine-rich splicing factor 7
38 zinc finger protein 644
39 tRNA methyltransferase 13 homolog (*S. cerevisiae*)
40 transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A)
41 cell division cycle 45 homolog (*S. cerevisiae*)
42 chromosome 17 open reading frame 80
43 regulator of G-protein signaling 5
44 high mobility group nucleosome binding domain 5
45 deoxynucleotidyltransferase, terminal, interacting protein 1
46 spindlin family, member 3
47 dihydrofolate reductase

1 jumonji domain containing 1C
2 ring finger protein 34, E3 ubiquitin protein ligase
3 thioredoxin-like 4B
4 calcium channel, voltage-dependent, alpha 2/delta subunit 1
5 origin recognition complex, subunit 1
6 heat shock 70kDa protein 9 (mortalin)
7 2-hydroxyacyl-CoA lyase 1
8 phosphoribosyl pyrophosphate synthetase 1
9 ataxin 1
10 RAD18 homolog (S. cerevisiae)
11 leucine rich repeat neuronal 4
12 deoxynucleotidyltransferase, terminal, interacting protein 1
13 centromere protein J
14 zinc finger protein 670
15 Rho GTPase activating protein 11A
16 complement component 3
17 tripartite motif containing 27
18 oral cancer overexpressed 1
19 cell division cycle 7 homolog (S. cerevisiae)
20 leucine rich repeat containing 34
21 nudix (nucleoside diphosphate linked moiety X)-type motif 16
22 nuclear factor (erythroid-derived 2)-like 2
23 solute carrier family 7 (anionic amino acid transporter light chain, xc- system), membe
24 family with sequence similarity 208, member B
25 lamin B receptor
26 FK506 binding protein 11, 19 kDa
27 ring finger protein, transmembrane 2
28 ariadne homolog 2 (Drosophila)
29 consortin, connexin sorting protein
30 chromosome 11 open reading frame 57
31 chromosome 6 open reading frame 147 /// KH homology domain containing 1
32 zinc finger protein 800
33 PHD finger protein 17
34 polymerase (RNA) II (DNA directed) polypeptide D
35 uncharacterized LOC339166 /// WSC domain containing 1
36 OTU domain containing 4
37 mature T-cell proliferation 1
38 B-cell CLL/lymphoma 11A (zinc finger protein)
39 carbohydrate (chondroitin 4) sulfotransferase 11
40 TNF receptor-associated factor 3
41 mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
42 protein kinase, AMP-activated, alpha 1 catalytic subunit
43 nucleoporin 160kDa
44 tripartite motif containing 27
45 Regulation of nuclear pre-mRNA domain containing 1A
46 antigen identified by monoclonal antibody Ki-67
47 basic, immunoglobulin-like variable motif containing

1 copine VIII
2 enhancer of zeste homolog 2 (Drosophila)
3 nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3
4 leucine zipper transcription factor-like 1
5 chemokine (C-X-C motif) ligand 5
6 dihydrofolate reductase
7 F-box protein 5
8 MAX gene associated
9 minichromosome maintenance complex component 5
10 ribosomal protein S6 kinase, 90kDa, polypeptide 3
11 X-ray repair complementing defective repair in Chinese hamster cells 4
12 nucleoporin 214kDa
13 peptidylprolyl isomerase F
14 sestrin 2
15 peptidase inhibitor 3, skin-derived
16 ChaC, cation transport regulator homolog 1 (E. coli)
17 chromodomain helicase DNA binding protein 1
18 copine VIII
19 zinc finger protein 830
20 choline kinase alpha
21 tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) pseudouridylate synthase 7
22 homolog (S. cerevisiae)-like
23 transmembrane protein 38B
24 HEAT repeat containing 6
25 tryptophanyl-tRNA synthetase
26 NHL repeat containing 2
27 pericentrin
28 tropomyosin 2 (beta)
29 HNRNPU antisense RNA 1 (non-protein coding)
30 dynein, cytoplasmic 2, heavy chain 1
31 queuine tRNA-ribosyltransferase domain containing 1
32 caspase 8, apoptosis-related cysteine peptidase
33 minichromosome maintenance complex component 4
34 exocyst complex component 6
35 Ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)
36 ATPase, aminophospholipid transporter, class I, type 8A, member 2
37 RB1-inducible coiled-coil 1
38 musashi homolog 2 (Drosophila)
39 uncharacterized LOC442075
40 consortin, connexin sorting protein
41 asparagine-linked glycosylation 1, beta-1,4-mannosyltransferase homolog (S. cerevisiae) glucuronidase, beta
42 pseudogene 1 /// glucuronidase, beta pseudogene 4
43 serine/arginine-rich splicing factor 1
44 family with sequence similarity 118, member A
45 FK506 binding protein 11, 19 kDa
46 chromodomain helicase DNA binding protein 1
47 N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2B

1 TIMELESS interacting protein
2 casein kinase 1, gamma 3
3 MAP7 domain containing 3
4 armadillo repeat containing 9
5 paternally expressed 10
6 7-dehydrocholesterol reductase
7 protein geranylgeranyltransferase type I, beta subunit
8 pseudouridylate synthase 7 homolog (S. cerevisiae)-like
9 ferrochelatase
10 gremlin 1
11 THO complex 5
12 TSC22 domain family, member 1
13 BCL2-associated transcription factor 1
14 DEAD (Asp-Glu-Ala-Asp) box polypeptide 10
15 uncharacterized LOC100287497 /// uncharacterized LOC100287934
16 dipeptidyl-peptidase 4
17 tRNA aspartic acid methyltransferase 1
18 methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate c
19 chromosome 18 open reading frame 25
20 transmembrane protein 209
21 leucine rich repeat neuronal 4
22 tRNA methyltransferase 6 homolog (S. cerevisiae)
23 heat shock 70kDa protein 14
24 DBF4 homolog (S. cerevisiae)
25 zinc finger and BTB domain containing 24
26 La ribonucleoprotein domain family, member 4
27 transducin (beta)-like 1X-linked
28 transmembrane protein 216
29 structural maintenance of chromosomes 3
30 Fanconi anemia, complementation group B
31 Chromatin licensing and DNA replication factor 1
32 HLA complex group 18 (non-protein coding)
33 POU class 2 homeobox 2
34 minichromosome maintenance complex component 3
35 DEP domain containing 1B
36 germ cell associated 2 (haspin)
37 ZNRD1 antisense RNA 1 (non-protein coding)
38 p21 protein (Cdc42/Rac)-activated kinase 2
39 ankyrin repeat domain 11
40 UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6
41 minichromosome maintenance complex component 4
42 malic enzyme 1, NADP(+)-dependent, cytosolic
43 uncharacterized LOC728855 /// uncharacterized LOC728875
44 PARP1 binding protein
45 ribonuclease H2, subunit B
46 uncharacterized LOC339166 /// WSC domain containing 1
47 golgi-associated PDZ and coiled-coil motif containing

1 gremlin 1
2 secretory carrier membrane protein 1
3 thymopoietin
4 LUC7-like 3 (S. cerevisiae)
5 RAD51 homolog B (S. cerevisiae)
6 chromosome 16 open reading frame 48
7 tudor and KH domain containing
8 bicaudal D homolog 1 (Drosophila)
9 glycyl-tRNA synthetase
10 tRNA methyltransferase 13 homolog (S. cerevisiae)
11 N(alpha)-acetyltransferase 16, NatA auxiliary subunit
12 UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6
13 zinc finger and BTB domain containing 24
14 elongation factor, RNA polymerase II, 2
15 thioredoxin reductase 1
16 acidic (leucine-rich) nuclear phosphoprotein 32 family, member E
17 transmembrane protein 182
18 discoidin domain receptor tyrosine kinase 2
19 O-linked N-acetylglucosamine (GlcNAc) transferase
20 uridine phosphorylase 1
21 chromosome 11 open reading frame 74
22 uncharacterized LOC400657
23 nuclear receptor subfamily 2, group C, member 1
24 family with sequence similarity 132, member B
25 junction mediating and regulatory protein, p53 cofactor
26 centrosome and spindle pole associated protein 1
27 adenomatous polyposis coli
28 acetyl-CoA acyltransferase 2
29 ion peptidase 1, mitochondrial
30 speckle-type POZ protein
31 thyroid hormone receptor interactor 13
32 denticleless E3 ubiquitin protein ligase homolog (Drosophila)
33 trafficking protein, kinesin binding 2
34 methyltransferase like 17
35 E1A binding protein p400
36 epoxide hydrolase 4
37 inhibitor of growth family, member 5
38 non-SMC element 4 homolog A (S. cerevisiae)
39 methyltransferase like 4
40 McKusick-Kaufman syndrome
41 rabaptin, RAB GTPase binding effector protein 1
42 zinc finger, CCHC domain containing 14
43 Mdm4 p53 binding protein homolog (mouse)
44 dyslexia susceptibility 1 candidate 1 /// DYX1C1-CCPG1 readthrough (non-protein coding)
45 RAP1 interacting factor homolog (yeast)
46 kelch-like 21 (Drosophila)
47 transmembrane protein 38B

1 uncharacterized LOC285628 /// microRNA 146a
2 chromosome 16 open reading frame 52
3 tRNA splicing endonuclease 15 homolog (S. cerevisiae)
4 nucleolar protein 9
5 golgi membrane protein 1
6 astrotactin 2
7 lin-7 homolog C (C. elegans)
8 F-box protein 5
9 PCF11, cleavage and polyadenylation factor subunit, homolog (S. cerevisiae)
10 mitochondrial fission process 1
11 GTP cyclohydrolase 1
12 distal-less homeobox 2
13 stimulated by retinoic acid gene 6 homolog (mouse)
14 replication factor C (activator 1) 5, 36.5kDa
15 UHRF1 binding protein 1
16 cleavage and polyadenylation specific factor 2, 100kDa
17 aldehyde dehydrogenase 1 family, member L2
18 protein arginine methyltransferase 6
19 activating transcription factor 1
20 MAX gene associated
21 RNA binding motif protein 26
22 mediator complex subunit 1
23 matrin 3 /// small nucleolar RNA host gene 4 (non-protein coding)
24 nucleoporin 153kDa
25 SUMO1/sentrin specific peptidase 1
26 nicotinamide phosphoribosyltransferase
27 target of EGR1, member 1 (nuclear)
28 centriolin
29 zinc finger protein 518B
30 paraspeckle component 1
31 methyltransferase like 17
32 nucleoporin 98kDa
33 non imprinted in Prader-Willi/Angelman syndrome 2
34 HAUS augmin-like complex, subunit 6
35 tripartite motif containing 27
36 interferon-related developmental regulator 1
37 heat shock transcription factor 2
38 serine/arginine-rich splicing factor 6
39 TWIST neighbor
40 cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa
41 abhydrolase domain containing 10
42 FGFR1 oncogene partner
43 Ribonuclease H1
44 proline-rich transmembrane protein 3
45 thiamin pyrophosphokinase 1
46 mitochondrial translational release factor 1
47 uncharacterized LOC728855 /// uncharacterized LOC728875

1 Ras homolog enriched in brain
2 heat shock 70kDa protein 9 (mortalin)
3 uncharacterized locus MGC21881
4 zinc finger, CCHC domain containing 9
5 intraflagellar transport 122 homolog (Chlamydomonas)
6 ADP-ribosylation factor-like 6
7 chromosome 5 open reading frame 44
8 ARP6 actin-related protein 6 homolog (yeast)
9 uncharacterized LOC728705
10 zinc finger protein 227
11 intercellular adhesion molecule 1
12 coiled-coil domain containing 41
13 upstream binding transcription factor, RNA polymerase I
14 Rho GTPase activating protein 26
15 MIS18 kinetochore protein homolog A (S. pombe)
16 MIS18 kinetochore protein homolog A (S. pombe)
17 Mdm1 nuclear protein homolog (mouse)
18 kelch repeat and BTB (POZ) domain containing 8
19 GC-rich sequence DNA-binding factor 1
20 biorientation of chromosomes in cell division 1
21 ribosomal protein S6 kinase, 90kDa, polypeptide 3
22 zinc finger and BTB domain containing 2
23 serine hydroxymethyltransferase 2 (mitochondrial)
24 F-box and leucine-rich repeat protein 20
25 PAN3 antisense RNA 1 (non-protein coding)
26 alpha-kinase 2
27 SSU72 RNA polymerase II CTD phosphatase homolog (S. cerevisiae)
28 ankyrin repeat domain 13C
29 four and a half LIM domains 1
30 ATPase, Ca++ transporting, plasma membrane 1
31 transportin 3
32 TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 140kDa
33 ankyrin repeat domain 11
34 unc-51-like kinase 4 (C. elegans)
35 leucine rich repeat containing 58
36 myoneurin
37 N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2B
38 nucleoporin 54kDa
39 methionyl-tRNA synthetase
40 Rho GTPase activating protein 26
41 NMDA receptor regulated 2
42 KIAA1549
43 proline and serine rich 1
44 ring finger protein 41
45 chromosome 5 open reading frame 43
46 methionyl-tRNA synthetase
47 RAB3A interacting protein (rabin3)

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RefSeq Transcript ID	FTSCi vs. FTSC		FTSCi vs. FTSCt	
	p-value	Fold-Change	p-value	Fold-Change
NM_031479	0.00063466	4.47907	0.00011722	-14.0452
NM_000237	0.0131274	1.76946	0.000156224	-13.4391
NM_001135058 /// NM_0040	0.0162055	1.61273	0.000153534	-10.6209
NM_005640 /// XM_0034036	0.0191241	1.58515	0.000178229	-10.0019
NM_001146335 /// NM_0180	0.0105459	2.59215	0.00102089	-8.43969
NM_013363	0.00305735	2.05335	0.00013755	-7.76648
NM_006902 /// NM_022716	0.00180276	1.87496	5.79E-05	-7.35897
NM_016354	0.000204472	3.5843	5.84E-05	-6.96513
NM_001146335 /// NM_0180	0.037793	3.59134	0.0127751	-6.82613
NM_152739 /// NR_029911 /	0.00976867	2.11093	0.000667088	-6.54988
NM_001198810 /// NM_0036	0.00449467	2.75125	0.000787765	-6.2531
NM_004418	0.00106929	1.67057	2.40E-05	-6.24194
NM_001146335 /// NM_0180	0.000211709	11.0668	0.000549682	-5.72656
NM_014832	0.0106757	1.93074	0.000634044	-5.68462
NM_006042	0.0122319	2.26689	0.00148915	-5.47793
NM_007193	0.00132816	3.27592	0.000495115	-5.23638
NM_001146335 /// NM_0180	6.25E-05	7.98439	0.000152631	-4.67199
NM_014832	0.000711087	1.69076	3.07E-05	-4.50536
NM_000885	0.00288285	3.6754	0.00192927	-4.45159
NM_021800 /// NM_201262	5.35E-05	4.09336	4.53E-05	-4.43831
NR_036540	0.012274	2.99782	0.00539301	-4.34267
NM_001561	0.000837259	5.11388	0.00114579	-4.33945
NM_014096 /// NM_017611 /	6.19E-05	6.44123	0.000127631	-4.31804
NM_001099282 /// NM_0010	0.00241823	2.46865	0.000594205	-4.28094
NM_014906 /// NR_048561	0.000575669	4.27946	0.000581963	-4.25678
NM_018099	0.000320981	8.46914	0.0010498	-4.19331
NM_021800 /// NM_201262	0.00428715	2.17319	0.000710089	-4.18842
NM_001205329 /// NM_0328	0.00415698	1.60154	0.000168486	-4.03007
NM_000885	0.000555189	2.75336	0.000222183	-3.96463
NM_000640	0.000156605	17.5483	0.00148009	-3.83944
NM_001165993 /// NM_0011	0.00291364	2.87724	0.00149129	-3.7743
NM_001136474 /// NM_0011	0.00194104	2.15487	0.000383515	-3.77305
NM_021800 /// NM_201262	0.000769521	5.86935	0.0018147	-3.75622
NM_001018111 /// NM_0053	0.000516371	1.67003	3.09E-05	-3.7319
NM_001008539 /// NM_0011	0.000240162	1.74941	1.89E-05	-3.69546
NM_013300	0.000539073	2.23343	0.00012699	-3.68719
NM_153360	0.00363714	1.82295	0.000372349	-3.67211
NR_026915	0.000325162	4.23953	0.000453272	-3.63997
NM_023070	0.000189272	3.33401	0.000155038	-3.6232
NM_001031855 /// NM_0247	2.13E-06	6.24795	6.21E-06	-3.60359
NM_001105515 /// NM_0058	0.0310334	1.56143	0.00161066	-3.57561
NM_020130	0.00166867	2.637	0.000750887	-3.5631
NM_001128174 /// NM_0033	0.0140875	1.92193	0.00211459	-3.55385

1	NM_001168683 /// NM_0183	0.0191046	1.78848	0.00210053	-3.54116
2	NM_004446	0.0331087	1.70171	0.00311908	-3.46836
3	NM_014096 /// NM_017611 /	0.000822018	2.98108	0.000560762	-3.46446
4	NR_027349 /// NR_027350 //,	0.00408478	3.68229	0.00503027	-3.36273
5	NM_018126	0.000693866	1.77011	7.43E-05	-3.34663
6	NM_001037293 /// NM_0530	0.000726468	3.8613	0.00101561	-3.34174
7	NM_000885	7.92E-05	11.8713	0.000704556	-3.28298
8	NM_001165993 /// NM_0011	0.0315555	1.62724	0.00261211	-3.28091
9	NM_138796	0.0113527	1.68461	0.00105663	-3.27148
10	NM_001006657 /// NM_0207	0.00772359	2.54	0.00416161	-3.17951
11	NM_004936 /// NM_078487	0.000250821	2.32403	9.85E-05	-3.16758
12	NM_016447	0.0279302	1.99346	0.00701231	-3.12972
13	NM_001163812 /// NM_0011	0.0210729	1.52625	0.00138443	-3.00133
14	NM_024758	0.000398925	3.28164	0.000503589	-3.00067
15	NM_004843	0.000288241	2.427	0.000154511	-2.98216
16	NM_001083588 /// NM_0010	0.0220728	1.8732	0.00483948	-2.94767
17	NM_001178091 /// NM_0011	0.00173067	2.39224	0.00092015	-2.94618
18	NR_001458 /// NR_030784	0.000105734	10.8253	0.00119618	-2.86971
19	NM_002451	0.00416762	1.66505	0.00049305	-2.8675
20	NM_144978	0.00866037	1.68121	0.00111525	-2.86529
21	NM_001012414	0.00112834	3.02887	0.00131713	-2.86223
22	NM_001193424 /// NM_0011	0.016303	1.92782	0.0043606	-2.85139
23	NM_002451	0.00969203	1.7786	0.00173004	-2.84699
24	NM_152435	0.00877474	1.55224	0.000710225	-2.83618
25	NM_001190463 /// NM_0019	0.000498646	14.2116	0.00771832	-2.82886
26	NM_001010853	0.0146196	1.79481	0.00284339	-2.82851
27	NM_001009913 /// NM_0012	0.000772337	2.98865	0.000901498	-2.82678
28	NM_004282	0.00473948	1.90698	0.00118131	-2.82492
29	NM_000071 /// NM_0011780	0.000188095	3.88182	0.000417843	-2.8229
30	NM_001134658 /// NM_1532	0.00486072	2.61877	0.00391508	-2.82248
31	NM_002033	0.0110379	1.90883	0.00286235	-2.81807
32	NM_003758	0.00505745	1.68683	0.000726672	-2.75615
33	NM_006252	0.000467916	1.9408	0.000131903	-2.75601
34	NM_000071 /// NM_0011780	0.00119818	3.01119	0.00156242	-2.73851
35	NM_020799	5.38E-05	6.6908	0.000360185	-2.73436
36	XR_109352 /// XR_109353 ///	0.009435	2.35498	0.00613506	-2.70979
37	NM_003799	0.00204196	2.23351	0.00108856	-2.70467
38	NM_001079877 /// NM_0069	0.0107778	1.58535	0.00118858	-2.68527
39	NM_001178091 /// NM_0011	0.000187637	6.60506	0.0013051	-2.67214
40	NM_014388	0.00306528	1.82265	0.000719961	-2.67015
41	NM_001104631 /// NM_0011	0.00816016	2.02134	0.00318482	-2.65505
42	NM_016567 /// NM_078468 /	0.00057257	2.18437	0.000296402	-2.65058
43	NM_024560	0.00644622	1.58069	0.000708264	-2.65027
44	NM_006321	0.00864154	1.57502	0.000952046	-2.63875
45	NM_020143	0.00823243	1.69414	0.0014386	-2.61813
46	NM_001127395 /// NM_1452	0.0433475	1.71245	0.00952125	-2.58109
47	NM_001080393	0.000330274	2.29404	0.000225712	-2.56861

1	NM_001127493 /// NM_0011	0.000125647	15.3348	0.00295129	-2.56258
2	NM_001004346 /// NM_0011	0.000227211	3.99391	0.000723962	-2.55525
3	NM_001166160 /// NM_0011	0.00349031	3.42279	0.0077023	-2.54484
4	NM_001080383 /// NM_0054	0.0124754	2.11209	0.0067535	-2.53415
5	NM_001166160 /// NM_0011	0.00145068	7.27677	0.0129271	-2.52925
6	XR_110828 /// XR_112106	0.00311139	1.85646	0.00095139	-2.52454
7	NM_001164750 /// NM_0011	0.0469918	1.85414	0.0164046	-2.51949
8	NM_003171	0.0369583	1.53649	0.0046082	-2.50101
9	NM_001178091 /// NM_0011	0.000450889	2.48127	0.00044943	-2.48373
10	NM_001002901	0.0101577	1.61988	0.00165711	-2.47034
11	NM_001172779 /// NM_0011	0.00571494	3.54471	0.0147565	-2.46736
12	NM_001010862 /// NR_02713	0.019748	1.79838	0.00610417	-2.44583
13	NM_003045	0.000313056	1.84303	0.000101403	-2.43956
14	NM_001048205 /// NM_0051	0.0197574	1.79332	0.00612467	-2.43318
15	NM_014167 /// NR_033192	0.0181265	1.53603	0.00230098	-2.42905
16	NM_001190463 /// NM_0019	0.000483805	26.5228	0.0210033	-2.42389
17	NM_005886	0.043365	1.75362	0.0131283	-2.41703
18	NM_004731	0.00252403	6.45052	0.0210054	-2.41337
19	NM_001042413 /// NM_1526	0.00547258	7.32928	0.0495364	-2.41334
20	NM_001001732 /// NM_0011	0.00452493	1.59394	0.000717432	-2.3953
21	NM_001178075 /// NM_0011	0.000135484	4.54944	0.000719672	-2.37491
22	NM_030971	0.0079964	1.60354	0.00139542	-2.3683
23	NM_001002269 /// NM_0160	0.0165645	1.56152	0.00258135	-2.35638
24	NM_025090	0.0123931	2.01927	0.00721546	-2.34397
25	NM_000189	0.00285691	2.0464	0.00172109	-2.34294
26	NM_018094	0.00265826	2.69731	0.00416898	-2.33937
27	NM_002687	0.0114346	2.13188	0.00827534	-2.33822
28	XR_109628 /// XR_112170	0.0179112	1.64274	0.0039839	-2.3309
29	NM_002349	0.00905109	1.81287	0.00333536	-2.32285
30	NM_001105573	0.0164246	1.82426	0.0063852	-2.32243
31	NM_000819 /// NM_0011360	0.000353907	2.16532	0.000273583	-2.32162
32	NM_014388	0.000115198	2.88666	0.000230481	-2.31745
33	NM_170710 /// NM_181265	0.00790502	1.73697	0.00235919	-2.3155
34	NM_022497	0.0119601	2.6073	0.017315	-2.31115
35	NM_020799	0.00241798	3.52234	0.00790851	-2.30453
36	NM_017645	0.0238987	2.32179	0.0245577	-2.30192
37	NM_002539	0.00459841	1.93659	0.00234236	-2.30165
38	NM_032226	0.049075	1.63478	0.0122774	-2.29743
39	NM_001201536 /// NM_0056	0.00417297	2.2937	0.00415649	-2.29631
40	NM_000390 /// NM_0010373	0.0381292	1.66308	0.010253	-2.29293
41	NM_001009894	0.0107222	1.55	0.00171921	-2.28709
42	NM_016331	0.00268468	1.69544	0.000723994	-2.27915
43	NM_006321	0.0146743	1.67168	0.00389625	-2.27202
44	NM_030647	0.00062285	3.53997	0.00225564	-2.26446
45	NM_001104631 /// NM_0011	0.023319	1.5898	0.00481276	-2.26296
46	NM_016000 /// NM_182916	0.00443791	1.83685	0.00188298	-2.26173
47	NM_138775	0.00560761	2.38545	0.00675275	-2.25843

1	NM_020143	3.14E-05	1.64671	7.23E-06	-2.25694
2	NM_152400	0.000981883	2.118	0.000786039	-2.24573
3	NM_182705	0.00130802	4.63123	0.00841306	-2.2405
4	NM_004731	0.00644407	3.02676	0.0156829	-2.23941
5	NM_004490	0.000596815	2.45693	0.000828983	-2.23592
6	NM_001042413 /// NM_1526	0.000702157	4.83719	0.00504626	-2.23493
7	NM_001253861 /// NM_0321	0.00425605	2.45158	0.00583942	-2.23304
8	NM_000310 /// NM_0011426	0.00428146	1.54817	0.000728238	-2.22407
9	NM_133465	0.0205419	2.42117	0.02691	-2.22294
10	NM_178836	0.000219836	3.52614	0.000853994	-2.22242
11	NM_001261392 /// NM_0012	0.0211745	1.69503	0.00678305	-2.21529
12	NM_018112	0.00526977	2.20697	0.00520709	-2.21427
13	NM_003201	0.00197535	1.84649	0.000935911	-2.20381
14	NM_001012626 /// NM_0226	9.72E-05	1.96184	6.05E-05	-2.20326
15	NM_003686 /// NM_006027 /	0.00254318	1.8947	0.00137272	-2.19998
16	NM_000534 /// NM_0011281	0.0108343	1.68593	0.00336926	-2.195
17	NM_001083585 /// NM_0047	0.00725004	2.66306	0.0136936	-2.18305
18	NM_001166160 /// NM_0011	0.0293561	1.6864	0.00986797	-2.1829
19	NM_003201	0.000383644	2.36409	0.000513794	-2.18133
20	NM_001105573	0.00580465	2.10916	0.00511808	-2.18094
21	NM_001197297 /// NM_0020	0.0357147	1.7551	0.0150079	-2.18066
22	NM_004589	0.00870461	1.66539	0.00257087	-2.17989
23	NM_017947	0.0145637	2.36319	0.0190643	-2.17961
24	NM_001004346 /// NM_0011	0.0441356	1.81415	0.0221481	-2.17653
25	NM_000946	0.00113159	1.94073	0.000712531	-2.17103
26	NM_000819 /// NM_0011360	0.0132359	2.04685	0.0106446	-2.16986
27	NM_018518 /// NM_182751	0.00384356	1.5335	0.000671021	-2.16921
28	NM_001160305 /// NM_0248	0.000518084	1.78333	0.000217428	-2.16889
29	NM_152547	0.0258773	1.55856	0.00563067	-2.15939
30	NM_001014972 /// NM_0012	0.00515123	2.42339	0.0076992	-2.15755
31	NM_018518 /// NM_182751	0.000594626	2.05625	0.000491883	-2.15631
32	NM_001008394	0.00112389	2.50578	0.00190546	-2.15513
33	NM_032367	0.000582068	2.56049	0.0010679	-2.15137
34	NM_001042490 /// NM_0010	0.00354691	1.72248	0.00129999	-2.15133
35	NM_002454 /// NM_024010	0.00890394	1.63759	0.00251837	-2.14901
36	NM_001515	0.000776009	2.0234	0.000616353	-2.14186
37	NM_001136557 /// NM_0011	0.0054936	2.33577	0.00753759	-2.13686
38	NM_001144920 /// NM_0011	0.00636774	2.90437	0.0164916	-2.13581
39	NM_006252	0.00218389	3.17969	0.0073931	-2.13527
40	NM_182705	3.13E-05	10.8573	0.000955389	-2.13526
41	NM_152405	0.00448527	5.04529	0.0363281	-2.13041
42	NM_001207025 /// NM_0012	2.09E-05	9.71903	0.000561762	-2.12836
43	NM_054027	0.00282206	2.14022	0.00289069	-2.12689
44	NM_002033	0.00186109	2.20711	0.00216835	-2.12016
45	NM_001256798 /// NM_0806	0.00134455	2.0951	0.00130972	-2.109
46	NM_006896	0.00355725	2.76325	0.00866587	-2.10634
47	NM_144695	0.0119262	1.74609	0.00528927	-2.10196

1	NM_001077708 /// NM_0196	0.00417888	2.19327	0.00491402	-2.10115
2	NM_030780	0.00276938	1.80031	0.00139815	-2.10067
3	NM_001203 /// NM_0012567	0.00038466	2.29274	0.000545195	-2.09164
4	NM_001032281 /// NM_0062	0.000200654	4.82939	0.00190125	-2.09143
5	NM_001077440 /// NM_0010	0.0274594	2.19617	0.0324525	-2.09126
6	NM_014285	0.0241844	1.68482	0.00937035	-2.09035
7	NM_002915 /// NM_181558	0.00933654	2.13383	0.0101011	-2.08961
8	NM_020386	0.0313722	1.64809	0.0109988	-2.08874
9	XR_110490 /// XR_133252	0.00680193	1.8571	0.00413322	-2.08819
10	NM_032367	8.40E-05	2.62677	0.000191925	-2.0804
11	NM_001178091 /// NM_0011	0.000144623	2.90728	0.000445728	-2.0787
12	NM_001207025 /// NM_0012	9.21E-05	5.97117	0.0013153	-2.07795
13	NM_001080393	0.0126859	2.64536	0.027539	-2.07554
14	NM_001207025 /// NM_0012	0.00680063	2.29608	0.00989971	-2.07066
15	NM_016612	0.000559677	2.28797	0.000820848	-2.06978
16	NM_001135575	0.00504942	1.85077	0.00315126	-2.0638
17	NM_144658	0.00324889	2.96744	0.0104124	-2.06236
18	NR_039993 /// NR_039994 //,	0.000798802	1.7685	0.000394067	-2.06104
19	NM_006646	0.00208229	2.47422	0.00401489	-2.0609
20	NR_040027 /// NR_040028	0.0273336	2.30729	0.0397199	-2.06071
21	NM_001166345 /// NM_0011	0.00200686	2.23524	0.00274159	-2.06057
22	NR_027301	0.00227337	1.89306	0.00159857	-2.05352
23	NM_001085379 /// NR_01543	0.00239448	3.83693	0.0143804	-2.04928
24	NM_001171904 /// NM_0147	0.00685567	1.73514	0.00324132	-2.04376
25	NM_001142853 /// NM_0186	0.0261356	2.3132	0.0395846	-2.04209
26	NM_152432	0.00693117	2.37481	0.0119164	-2.04114
27	NM_198461	4.92E-05	6.3997	0.000865848	-2.03385
28	NM_017518 /// NM_080701 /	0.0171989	1.70603	0.00780566	-2.03308
29	NM_001203 /// NM_0012567	3.37E-05	3.30775	0.000161656	-2.03033
30	NM_001098729 /// NR_03341	0.013009	1.67437	0.00534859	-2.02602
31	NM_001165412 /// NM_0039	0.0263847	1.53305	0.00662263	-2.02483
32	NM_003201	0.000256245	2.32318	0.000440958	-2.01887
33	NM_001164271 /// NM_0060	0.0106211	2.59132	0.0243686	-2.0186
34	NM_181655 /// NM_181656	0.0167084	1.75939	0.00913869	-2.01825
35	NM_000077 /// NM_0011951	0.000168763	7.01954	0.00354181	-2.0063
36	NM_001134830 /// NM_0011	0.00869819	1.55571	0.00235448	-2.00496
37	NM_006896	0.000201778	2.67862	0.000572769	-2.00204
38	NM_198461	3.84E-05	22.0423	0.00325389	-2.00145
39	NM_001018054 /// NM_0046	0.000560213	3.37963	0.00294346	-2.00087
40	NM_005746 /// NM_182790	0.00119964	1.84134	0.000823987	-2.00003
41	NM_001172574 /// NM_0011	0.00357842	2.64825	0.00961033	-1.99265
42	NM_001174166 /// NM_0046	0.000282538	10.8481	0.0106255	-1.99179
43	NM_001105206 /// NM_0011	0.000932597	3.98443	0.00713946	-1.98873
44	NM_001039374 /// NM_0328	0.0484309	1.60599	0.0184728	-1.98795
45	NM_001086	0.00117923	2.56199	0.00296999	-1.98723
46	NM_152407	0.00584519	1.9184	0.00503191	-1.98656
47	NM_006291	0.0239911	1.69711	0.0118079	-1.98624
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1	NM_001173982 /// NM_0184	0.00309543	2.4425	0.00666285	-1.98279
2	NM_021154 /// NM_058179	0.000333293	3.97112	0.00267196	-1.97768
3	NM_016612	0.000586904	2.4747	0.00136289	-1.97719
4	NM_003201	0.0439704	1.88703	0.0370734	-1.97305
5	NR_003013 /// NR_027058	0.0257217	1.50758	0.00648756	-1.96633
6	NM_001197330 /// NM_0011	0.00482758	1.92208	0.00439507	-1.96409
7	NM_001616	0.00350817	2.24288	0.00594764	-1.95935
8	NM_174910	0.0200911	2.20908	0.0312244	-1.95576
9	NM_014053	0.0186546	1.68485	0.0093172	-1.95549
10	NM_001006622 /// NM_0010	0.00107238	2.42015	0.0024207	-1.95444
11	NM_001013620	0.00217616	1.73438	0.00122479	-1.95327
12	XR_110082 /// XR_112807	0.0221781	1.60864	0.00865756	-1.95219
13	NM_016612	0.00773949	2.00224	0.00862817	-1.95053
14	NM_000201	0.00309128	2.79164	0.0106017	-1.94901
15	NM_144581	0.000102546	3.54868	0.000693825	-1.94833
16	NM_000462 /// NM_130838 /	0.00704445	1.61659	0.00273909	-1.94722
17	NM_001142317 /// NM_0011	0.0383444	1.66657	0.0191852	-1.94489
18	NM_032834	0.0274376	1.84453	0.0220436	-1.94446
19	NM_000636 /// NM_0010244	3.77E-05	2.85524	0.000147745	-1.94376
20	NM_017754	0.000488602	1.98071	0.000531843	-1.943
21	NM_005916 /// NM_182776	0.00779986	2.03222	0.00943362	-1.94049
22	NM_024094	0.017065	1.89181	0.0153526	-1.94001
23	NM_001935	0.00455235	2.67987	0.0140541	-1.93798
24	NM_002577	0.00377446	1.6124	0.00146981	-1.93398
25	NM_014363	0.0013257	2.31108	0.00268266	-1.93257
26	NM_001139459 /// NM_1526	0.00617942	2.5087	0.0158372	-1.92984
27	NM_000077 /// NM_0011951	0.000190417	7.25995	0.00494034	-1.92962
28	NM_000436	0.000651287	2.86629	0.00263556	-1.92577
29	NM_006513 /// NR_034072 //	0.0056111	1.79146	0.00402468	-1.92384
30	NM_002041 /// NM_005254 /	0.000100156	2.26795	0.000196162	-1.92308
31	NM_001135575	0.0193521	1.85311	0.0165331	-1.92265
32	NM_001144958 /// NM_0011	0.000697593	5.25193	0.0105706	-1.91701
33	NM_014388	0.000936701	1.88016	0.000858169	-1.91614
34	NM_020768	0.00272467	3.71416	0.0199622	-1.9132
35	NM_001199237 /// NM_0011	0.000926021	2.5158	0.00261223	-1.91269
36	NM_003455	0.013143	1.57998	0.00489996	-1.91243
37	NM_004731	0.0130712	2.43743	0.0308082	-1.91089
38	NM_203302 /// NM_203477 /	0.000159165	1.7799	0.000113582	-1.90687
39	NM_001018054 /// NM_0046	0.00616657	3.4043	0.0354931	-1.9068
40	NM_001256279 /// NM_0012	6.05E-05	2.02469	8.00E-05	-1.90118
41	NM_001012626 /// NR_02684	0.000870614	1.76875	0.000611444	-1.90111
42	NM_001080502 /// NM_1734	0.000408825	3.92294	0.00380936	-1.89794
43	NM_003090	0.0108517	1.61247	0.00472607	-1.89672
44	NM_001034841 /// NR_02802	0.00298622	2.0228	0.00395149	-1.89592
45	NM_001145343 /// NM_0011	0.00200145	2.08265	0.00299097	-1.8954
46	NM_007192	0.000705093	2.23633	0.00139672	-1.89411
47	NM_001032281 /// NM_0062	3.02E-05	6.08242	0.000673972	-1.89288

1	NM_001018113 /// NM_1526	0.00150255	1.99361	0.00189164	-1.89263
2	NM_001201545 /// NM_0227	0.0119035	1.625	0.00550624	-1.892
3	NM_032021	0.0154009	1.58713	0.00624072	-1.8917
4	NM_002895 /// NM_183404	0.0183636	2.13769	0.0294375	-1.88929
5	NM_002395	3.00E-05	2.60211	0.000102531	-1.88592
6	NM_001034841 /// NR_02802	0.0259175	1.55097	0.00953271	-1.88309
7	NM_003146	0.000209737	1.50377	5.65E-05	-1.88245
8	NM_014388	0.00113928	3.37772	0.00764186	-1.88216
9	NM_001173982 /// NM_0184	0.00572589	2.3187	0.0128437	-1.88065
10	NM_001008708	0.00334497	1.65398	0.00172212	-1.88037
11	NM_001127395 /// NM_1452	0.00128205	3.74853	0.0109021	-1.87733
12	NM_024796 /// NR_024321	0.031931	1.86897	0.031635	-1.8732
13	NM_001139466 /// NM_0011	0.017598	1.6328	0.00890239	-1.87189
14	NM_001190809 /// NM_0219	0.0463433	1.53892	0.0174776	-1.87163
15	NM_001193621 /// NM_0011	0.0126846	1.99025	0.0164528	-1.87045
16	NM_005916 /// NM_182776	0.000992709	2.45556	0.00287333	-1.86959
17	NM_017664	0.000370882	2.00879	0.000516562	-1.86644
18	NM_001031713 /// NM_0221	0.000458761	1.96481	0.000584997	-1.86333
19	NM_032315	0.000805887	4.02767	0.00845967	-1.86118
20	NM_019022	0.0245526	1.86152	0.0246548	-1.85971
21	NM_030647	0.00028182	2.17909	0.000559878	-1.85614
22	NM_001128431 /// NM_0011	6.49E-05	2.7236	0.000274985	-1.85559
23	NM_004671 /// NM_173206	0.0183079	1.78304	0.0153033	-1.85452
24	NM_002915 /// NM_181558	0.000594384	1.82594	0.000551192	-1.85444
25	NM_024524	0.00873766	1.78379	0.00733656	-1.85074
26	NM_001193424 /// NM_0011	0.00226284	2.00991	0.00326604	-1.85073
27	XR_110202 /// XR_112909	0.0413879	1.74915	0.0325229	-1.84912
28	NM_005687	0.0042141	1.69261	0.00269165	-1.84799
29	NM_001142307 /// NM_0053	0.0282895	2.01099	0.0395128	-1.84677
30	NR_024490	0.00434356	2.43428	0.0125446	-1.84438
31	NM_153006	0.00761652	1.75613	0.00601922	-1.84339
32	NM_014243	5.44E-05	16.2957	0.00488404	-1.84266
33	NM_001013694	0.0299976	1.6025	0.0150155	-1.84165
34	NM_001083585 /// NM_0047	0.00365219	1.69364	0.00238021	-1.84099
35	NM_001010986 /// NM_1736	0.0125925	1.66801	0.00767837	-1.8409
36	NR_024278	0.00323011	3.55994	0.0253577	-1.83766
37	NM_016310	0.00147305	1.77277	0.00123507	-1.83639
38	XR_109888 /// XR_112387	0.00900851	2.28238	0.0210662	-1.83364
39	NM_006951	0.00115453	2.97818	0.0064552	-1.8301
40	NM_001014437 /// NM_0010	0.00103995	2.93184	0.00563151	-1.82776
41	NM_001139459 /// NM_1526	0.00119169	1.94527	0.00159693	-1.82667
42	NM_001444	0.0036916	1.74034	0.00290451	-1.82528
43	NM_001137673 /// NM_0045	0.0130936	1.73643	0.0104308	-1.81992
44	NM_152446	0.000827576	1.65327	0.000493012	-1.81957
45	NM_001143781 /// NM_0011	0.00365265	1.81068	0.00357012	-1.81921
46	NM_001789 /// NM_201567	0.00535963	1.87875	0.00623226	-1.81894
47	NM_001032283 /// NM_0010	0.0099983	2.48869	0.0313207	-1.81869
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1	NM_001159728 /// NM_0169	0.00504254	2.07935	0.00900596	-1.81704
2	NM_001039618 /// NM_0212	0.0036308	1.59194	0.00174923	-1.81671
3	NM_013319	0.00141553	2.47236	0.00477727	-1.81593
4	NM_001134937 /// NM_0011	0.0175268	1.96028	0.0247206	-1.80784
5	NM_006951	0.000491373	1.82314	0.000512932	-1.80751
6	NM_018063	0.00159234	2.03713	0.00273354	-1.80709
7	NM_152608	0.00640093	1.52105	0.00237011	-1.80619
8	NM_014165	0.00232924	2.56104	0.00887638	-1.80577
9	NM_022466	0.00381566	2.21183	0.0088876	-1.80533
10	NM_001193609 /// NM_0011	0.00045316	2.03874	0.000790303	-1.80521
11	NM_001142307 /// NM_0053	0.00156257	1.96614	0.00233356	-1.80347
12	NM_018063	0.000368249	2.99828	0.0023154	-1.80338
13	NM_005729	0.000146035	2.67279	0.000670943	-1.80276
14	NM_001242804	0.0133752	1.69119	0.0097206	-1.80251
15	NM_001106	0.00312453	1.8511	0.00356913	-1.80079
16	NR_024284	0.0152437	1.96773	0.0223481	-1.79982
17	NM_007007	0.00529879	1.60638	0.00285093	-1.79886
18	NM_020401	0.000500381	1.51046	0.000174783	-1.79845
19	NM_005680	0.00746063	1.72308	0.00601599	-1.79821
20	NM_001098616 /// NM_0154	0.00216243	1.79763	0.0021704	-1.79631
21	NM_001134779 /// NM_0163	0.00742928	2.04842	0.0131235	-1.79577
22	NM_001128324 /// NM_1748	0.00387258	1.75824	0.0034822	-1.79567
23	NM_001080415	0.00193267	1.72988	0.00159463	-1.79519
24	NM_001080415	0.0275171	1.70059	0.0214421	-1.79207
25	NM_001077204 /// NM_0247	0.000414536	1.63822	0.00025334	-1.79016
26	NM_001014437 /// NM_0010	0.00147774	1.9716	0.00232027	-1.78987
27	NM_001143787 /// NM_0011	0.0375945	1.52269	0.0159601	-1.78858
28	NM_001102592 /// NM_1445	0.0131974	2.39366	0.038906	-1.78808
29	NM_001134375 /// NM_0011	0.00483676	2.27121	0.0129339	-1.78507
30	NM_001193609 /// NM_0011	0.000639126	1.76237	0.000600254	-1.78383
31	NM_001008544 /// NM_1382	0.00179313	1.57872	0.000895636	-1.78204
32	NM_014881	0.0083243	1.55125	0.0037942	-1.78174
33	NM_001256054 /// NM_0183	0.0250256	1.57874	0.0135148	-1.77418
34	NM_004419	0.00363267	1.61607	0.00216495	-1.77401
35	NM_016612	0.00112256	1.72073	0.000955853	-1.77372
36	NM_001160147 /// NM_0011	0.000472704	4.05912	0.00653089	-1.77135
37	NM_001031684 /// NM_0011	0.00210986	1.51413	0.000821038	-1.77068
38	NM_016620 /// NM_032186 /	0.00989997	2.08711	0.019963	-1.76887
39	NM_019083	0.0114498	1.60526	0.00688425	-1.76279
40	NM_003198	0.0165819	1.55885	0.00842437	-1.76188
41	NM_001178010 /// NM_0011	0.0092612	1.91559	0.0136506	-1.76051
42	NM_001100621 /// NM_0011	0.0346992	1.74329	0.0334822	-1.75693
43	NM_001195303 /// NM_0012	0.0253672	1.68584	0.0209954	-1.75193
44	NM_030763	0.00369573	4.0031	0.0442541	-1.75154
45	NM_052951	0.00136162	2.18801	0.00363971	-1.7499
46	NM_001010862 /// NR_02713	0.00169036	1.52532	0.000735697	-1.74987
47	NM_000791	0.00642775	2.07509	0.0137892	-1.74437

1	NM_004241 /// NM_032776	0.00166799	1.93903	0.00278747	-1.74316
2	NM_001256858 /// NM_0251	0.0404806	1.52725	0.0199748	-1.74217
3	NM_001142317 /// NM_0011	0.00924718	1.95634	0.0156716	-1.74199
4	NM_000722	1.30E-05	38.0977	0.00348667	-1.74171
5	NM_001190818 /// NM_0011	0.00860468	1.5317	0.00405029	-1.7417
6	NM_004134	0.0117181	1.55151	0.00606868	-1.74101
7	NM_012260	0.00290217	2.14489	0.00729344	-1.74057
8	NM_001204402 /// NM_0027	0.00853284	2.00231	0.0160781	-1.73828
9	NM_000332 /// NM_0011281	0.00269869	2.28074	0.00853174	-1.73781
10	NM_020165	0.0315474	1.69728	0.0282551	-1.73659
11	NM_152611	4.59E-05	4.52487	0.000923935	-1.73649
12	NM_052951	0.00606517	2.67105	0.029733	-1.73537
13	NM_018451 /// NR_047594 //	0.0175583	1.74854	0.0182311	-1.73515
14	NM_001204220 /// NM_0332	0.0125593	2.44709	0.0453621	-1.73403
15	NM_014783 /// NM_199357	0.00769013	2.5401	0.0324139	-1.73299
16	NM_000064	0.00355541	1.96417	0.006431	-1.73237
17	NM_006510 /// NM_030950	0.00211844	3.23793	0.0184004	-1.73212
18	NM_153451	0.0289648	1.89263	0.0429436	-1.72773
19	NM_001134419 /// NM_0011	5.65E-05	2.63167	0.000311532	-1.72739
20	NM_001172779 /// NM_0011	0.000528157	5.2077	0.013053	-1.72721
21	NM_001171905 /// NM_0011	0.00707567	1.78235	0.00833693	-1.72539
22	NM_001145412 /// NM_0011	0.00832441	1.64225	0.00638456	-1.72395
23	NM_014331	6.62E-05	4.30096	0.00124993	-1.72278
24	NM_017782	0.00010423	1.60986	7.01E-05	-1.72223
25	NM_002296 /// NM_194442	0.000411947	2.02286	0.000889547	-1.72223
26	NM_001143781 /// NM_0011	0.00260635	2.18932	0.00754754	-1.71933
27	NM_001109903 /// NM_0328	0.00371185	2.50893	0.0165883	-1.71871
28	NM_006321	0.00109128	2.18544	0.00321099	-1.7181
29	NM_001139459 /// NM_1526	0.002444859	2.99384	0.0182448	-1.71669
30	NM_001082969 /// NM_0010	0.00438994	1.69415	0.00409822	-1.7158
31	NM_001251874 /// NM_0305	0.00492145	2.24465	0.0154618	-1.71352
32	NM_176814	0.00516958	2.31341	0.0179284	-1.71303
33	NM_024900 /// NM_199320	0.000255248	2.5024	0.00124823	-1.71168
34	NM_004805	0.005666	1.85344	0.00840095	-1.71141
35	NM_015253 /// NR_040000	0.00142723	4.60425	0.0274714	-1.71101
36	NM_001102653 /// NM_0174	0.00131332	1.86767	0.00205051	-1.71065
37	NM_001018025 /// NM_0142	0.0157457	1.71212	0.0159134	-1.70857
38	NM_018014 /// NM_022893 /	0.00211537	1.78254	0.00264463	-1.70839
39	NM_001173982 /// NM_0184	0.0012245	1.94519	0.00232428	-1.70749
40	NM_001199427 /// NM_0033	0.00263809	2.81082	0.0171842	-1.70595
41	NM_000251 /// NM_0012582	0.00106095	3.04204	0.00894201	-1.70535
42	NM_006251 /// NM_206907	0.019139	1.53015	0.0102487	-1.70508
43	NM_015231	0.0163949	1.67072	0.0148802	-1.7019
44	NM_006510 /// NM_030950	0.00218253	1.92518	0.00400657	-1.70183
45	NM_018170	0.0177584	1.5139	0.00894518	-1.70086
46	NM_001145966 /// NM_0024	0.00185411	2.00857	0.00410547	-1.70064
47	NM_001159596 /// NM_0176	0.00363329	1.80339	0.00494098	-1.69919

1	NM_153634	0.0221291	1.61245	0.0167226	-1.69891
2	NM_001203247 /// NM_0012	0.00237953	2.07387	0.00603748	-1.69697
3	NM_004555 /// NM_173163 /	0.0152631	1.50384	0.00739849	-1.69673
4	NM_020347	0.000918209	3.37897	0.0103347	-1.69619
5	NM_002994	2.71E-06	12.0184	0.000280904	-1.69515
6	NM_000791	0.00441778	1.61409	0.00333263	-1.69505
7	NM_001142522 /// NM_0121	6.01E-05	3.38543	0.000731044	-1.69497
8	NM_001080541 /// NM_0011	0.0129366	1.68203	0.0124364	-1.69461
9	NM_006739	0.00320447	2.72489	0.0196566	-1.69389
10	NM_004586	0.00166508	2.52393	0.00849562	-1.69389
11	NM_003401 /// NM_022406 /	0.0356335	1.68864	0.0351692	-1.6932
12	NM_005085	0.0123252	2.00648	0.0263621	-1.69214
13	NM_005729	0.00357951	2.03123	0.00841882	-1.69191
14	NM_031459	8.73E-06	3.27526	9.98E-05	-1.6919
15	NM_002638	0.00254981	1.81461	0.00367393	-1.69147
16	NM_001142776 /// NM_0241	0.000829706	2.80573	0.00597604	-1.69036
17	NM_001270	0.0135032	1.55468	0.00832783	-1.68966
18	NM_153634	0.00130352	1.59953	0.00094246	-1.68912
19	NM_052857	0.000598746	2.08272	0.00161825	-1.68909
20	NM_001277 /// NM_212469	0.0174426	1.71927	0.0191285	-1.68837
21	NM_001032281 /// NM_0062	0.000188797	7.88497	0.0105257	-1.68736
22	NM_001098614 /// NM_0010	0.00523292	1.95401	0.0105624	-1.68713
23	NM_018112	0.000860555	3.93473	0.0139011	-1.68668
24	NM_022070	0.00282419	2.05795	0.00719791	-1.68489
25	NM_004184 /// NM_173701 /	0.00113803	2.47219	0.00570311	-1.68353
26	NM_198514	0.019546	1.79881	0.0269358	-1.6829
27	NM_006031	0.000130649	1.86546	0.000224709	-1.682
28	NM_001145822 /// NM_0032	0.00512921	1.64219	0.00449919	-1.68056
29	NR_026778	1.61E-05	2.83353	0.000130566	-1.6784
30	NM_001080463 /// NM_0013	0.0131662	2.06531	0.0325128	-1.67807
31	NM_001256835 /// NM_0012	0.0202259	1.57991	0.0145372	-1.67595
32	NM_001080124 /// NM_0010	0.00757413	1.59597	0.00571781	-1.67517
33	NM_005914 /// NM_182746	0.00224807	2.55083	0.012417	-1.67476
34	NM_001013848 /// NM_0190	0.00507779	2.79705	0.0340014	-1.6736
35	NM_004181	0.000509403	6.333	0.0202006	-1.67308
36	NM_016529	0.00148143	4.27085	0.0280921	-1.66988
37	NM_001083617 /// NM_0147	0.00470432	2.04435	0.0120891	-1.66964
38	NM_138962 /// NM_170721	0.00327522	1.76125	0.00436779	-1.66944
39	NM_001013730 /// XR_11003	0.00108092	1.82484	0.00173326	-1.66939
40	NM_001139459 /// NM_1526	0.00103627	2.0421	0.00276046	-1.66789
41	NM_019109	0.0104462	1.66241	0.0102678	-1.66763
42	NM_206908 /// NM_206910 /	0.00309836	3.4743	0.036553	-1.66696
43	NM_001078166 /// NM_0069	0.00596351	2.72094	0.0373696	-1.66662
44	NM_001104595 /// NM_0179	0.040242	1.50648	0.02288	-1.66433
45	NM_001143781 /// NM_0011	0.000119242	2.22396	0.000460359	-1.66234
46	NM_001270	0.0104605	1.56989	0.00751516	-1.66051
47	NM_001079516	0.0122345	1.51327	0.00695521	-1.65922

1	NM_017858	8.36E-05	2.8939	0.00076407	-1.65855
2	NM_001031812 /// NM_0010	0.007085	1.58938	0.00553073	-1.65749
3	NM_001173516 /// NM_0011	0.00301623	1.68215	0.00329285	-1.65636
4	NM_025139	0.000522525	2.39766	0.00265146	-1.6558
5	NM_001040152 /// NM_0011	0.00889404	1.52309	0.00534599	-1.65388
6	NM_001163817 /// NM_0013	0.00103094	1.7197	0.00128769	-1.65338
7	NM_005023	0.0499922	1.50536	0.0297021	-1.65308
8	NM_001098614 /// NM_0010	0.0283779	1.75716	0.0382835	-1.65168
9	NM_000140 /// NM_0010125	0.00551416	2.68166	0.0351708	-1.65136
10	NM_001191322 /// NM_0011	0.000106886	50.8321	0.0397859	-1.64969
11	NM_001002877 /// NM_0010	0.000192821	1.64532	0.000190454	-1.64872
12	NM_001243797 /// NM_0012	0.000941362	1.94697	0.00219855	-1.64798
13	NM_001077440 /// NM_0010	0.0013272	1.53702	0.00085622	-1.64634
14	NM_004398	0.00052048	1.62292	0.000478289	-1.64575
15	XR_108279 /// XR_112047 ///	0.0104249	1.57177	0.00798216	-1.64406
16	NM_001935	7.91E-05	6.11185	0.0036534	-1.64306
17	NM_004412 /// NM_176081 /	0.00711549	1.82473	0.01232	-1.64014
18	NM_001040409 /// NM_0066	0.000631878	2.14286	0.00226537	-1.63958
19	NM_001008239 /// NM_1450	0.0137383	1.65586	0.0145337	-1.63906
20	NM_032842	0.0107478	1.74967	0.015165	-1.63894
21	NM_152611	0.000666062	5.40575	0.0226232	-1.63829
22	NM_015939	0.00057903	2.36385	0.00297932	-1.63789
23	NM_016299	0.000109506	2.23772	0.000472804	-1.63774
24	NM_006716	0.0123603	1.9703	0.0293555	-1.63582
25	NM_001164313 /// NM_0147	0.0137991	1.74063	0.0191052	-1.63559
26	NM_001170803 /// NM_0011	0.0037431	1.63921	0.00381259	-1.63409
27	NM_001139466 /// NM_0011	0.00357547	2.1757	0.0132659	-1.63248
28	NM_001173990 /// NM_0011	0.01664	1.84696	0.0304416	-1.63091
29	NM_005445	0.00537066	1.7746	0.00848283	-1.62995
30	NM_001018113 /// NM_1526	0.00367366	2.27655	0.0160643	-1.6296
31	NM_030928	0.0152226	1.98623	0.037632	-1.62838
32	NR_024052 /// NR_024053	0.00537728	1.97238	0.0138662	-1.62488
33	NM_001207025 /// NM_0012	0.0107659	1.95274	0.025965	-1.62306
34	NM_001270472 /// NM_0023	0.000600553	1.65122	0.000667928	-1.62234
35	NM_001145208 /// NM_0183	0.000118241	2.01724	0.000359774	-1.6215
36	NM_031965	0.0252189	1.74973	0.0369458	-1.62073
37	NR_026751	0.00237003	1.7446	0.0036181	-1.61818
38	NM_002577	0.00495906	1.94867	0.0125831	-1.61625
39	NM_001256182 /// NM_0012	6.41E-05	1.89987	0.000152827	-1.61621
40	NM_004775	0.0223901	1.76316	0.0347124	-1.61546
41	NM_005914 /// NM_182746	0.00283966	1.72623	0.00414281	-1.61503
42	NM_002395	0.002179	2.6167	0.0158853	-1.61491
43	NR_024510 /// NR_024511 //,	0.00172778	1.51711	0.00114811	-1.61417
44	NM_017915	0.00130469	2.75527	0.0114425	-1.61225
45	NM_001142279 /// NM_0245	0.0229905	1.70632	0.0309477	-1.61157
46	NM_015253 /// NR_040000	8.54E-05	26.9902	0.0236274	-1.61027
47	NM_001017408 /// NM_0203	0.0115488	1.80308	0.0207582	-1.6094
48					
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1	NM_001191322 /// NM_0011	5.15E-05	76.117	0.0311946	-1.60915
2	NM_004866 /// NM_052822	4.40E-05	1.93861	0.000118744	-1.608
3	NM_001032283 /// NM_0010	0.00227181	2.71931	0.0188701	-1.60735
4	NM_006107 /// NM_016424	0.000386463	2.20595	0.00175654	-1.60715
5	NM_002877 /// NM_133509 /	0.018019	1.97662	0.0464021	-1.60588
6	NM_032140	0.00916668	1.93274	0.0227439	-1.6054
7	NM_001083963 /// NM_0010	0.00501599	2.09443	0.0175528	-1.60507
8	NM_001003398 /// NM_0017	0.000280885	3.36166	0.00449885	-1.60494
9	NM_002047	0.000946222	2.11967	0.00367965	-1.60458
10	NM_019083	0.00423235	1.78707	0.00764793	-1.60358
11	NM_001110798 /// NM_0185	0.000832492	1.59086	0.000795325	-1.60237
12	NM_004775	0.000362299	1.90075	0.000928323	-1.59658
13	NM_001164313 /// NM_0147	0.0255384	1.59839	0.0257641	-1.5959
14	NM_012081	0.00323475	2.11084	0.0123573	-1.59498
15	NM_001093771 /// NM_0012	4.13E-05	8.99296	0.00407913	-1.59493
16	NM_001136478 /// NM_0011	0.000734595	2.82448	0.0075681	-1.59478
17	NM_144632	0.00240364	2.35309	0.0136059	-1.59436
18	NM_001014796 /// NM_0061	0.000520656	6.27733	0.0264631	-1.59393
19	NM_003605 /// NM_181672 /	0.000508023	1.6757	0.000687834	-1.59386
20	NM_003364 /// NM_181597	0.00265557	2.34934	0.0149272	-1.59332
21	NM_138787	0.00296121	1.63932	0.00352625	-1.59276
22	NM_001008234 /// NR_02448	0.000320415	3.53015	0.00601853	-1.59176
23	NM_001032287 /// NM_0011	0.000420976	2.07731	0.00161403	-1.59103
24	XM_001714385 /// XM_00311	2.88E-05	9.15728	0.00303332	-1.5878
25	NM_152405	8.15E-05	9.1873	0.00828246	-1.58706
26	NM_001077204 /// NM_0247	0.0145693	1.76857	0.0259793	-1.58421
27	NM_000038 /// NM_0011275	0.00674162	1.92199	0.0179673	-1.58359
28	NM_006111	0.00156352	2.04789	0.00572152	-1.58239
29	NM_004793	0.00346314	1.72581	0.00577156	-1.57957
30	NM_001007226 /// NM_0010	0.0026938	2.03545	0.00957133	-1.57937
31	NM_001166260 /// NM_0042	0.00529259	1.67224	0.00745869	-1.57771
32	NM_016448	0.00135977	3.98727	0.03116	-1.57769
33	NM_015049	0.00124878	2.95563	0.0150773	-1.57685
34	NM_001029991 /// NM_0010	0.0171706	1.55831	0.0160766	-1.57529
35	NM_015409	2.42E-05	1.78756	5.05E-05	-1.57484
36	NM_173567	6.23E-06	9.4035	0.000737304	-1.57438
37	NM_032329	0.00612027	1.80054	0.0127157	-1.57413
38	NM_001167865 /// NM_0176	0.000546436	1.58533	0.000578037	-1.5717
39	NM_022840	0.00643627	2.62669	0.0498256	-1.56984
40	NM_018848 /// NM_170784 /	0.0013799	1.54533	0.0012515	-1.56814
41	NM_001083585 /// NM_0047	0.00193077	2.00724	0.0068685	-1.56769
42	NM_015144	0.00255357	2.18269	0.0124072	-1.56692
43	NM_001204171 /// NM_0012	0.0214313	1.66534	0.0300506	-1.56633
44	NM_001033559 /// NM_0010	0.00112725	2.62133	0.0103144	-1.56606
45	NM_001177663 /// NM_0011	0.00764503	2.01539	0.0260536	-1.56604
46	NM_014851	0.00106237	2.05077	0.00424374	-1.5644
47	NM_018112	0.000131887	2.47014	0.001073	-1.56375

1	NR_029701	1.41E-05	58.2943	0.00964676	-1.56329
2	NM_001164579 /// NM_1735	0.00210682	1.64981	0.0029661	-1.56104
3	NM_001127394 /// NM_0529	0.000982904	2.50736	0.00810435	-1.5605
4	NM_024654	0.00250936	1.56349	0.00254453	-1.56017
5	NM_001099268 /// NM_0165	0.00624792	1.61565	0.00780779	-1.55831
6	NM_001184734 /// NM_0011	0.00366277	1.68807	0.00592798	-1.55741
7	NM_018362	0.0115955	1.60991	0.0141787	-1.55711
8	NM_001142522 /// NM_0121	0.000286638	3.54316	0.00627161	-1.55686
9	NM_015885	0.0139305	1.51452	0.0117431	-1.55502
10	NM_001003704 /// NM_0164	0.00488028	1.75017	0.00960255	-1.55469
11	NM_000161 /// NM_0010240	3.25E-05	4.40449	0.00121078	-1.55398
12	NM_004405	0.000328844	11.3929	0.0423437	-1.55369
13	NM_001142617 /// NM_0011	0.0193205	1.63007	0.0255378	-1.55294
14	NM_001130112 /// NM_0011	0.00960025	1.67088	0.0147588	-1.55238
15	NM_017754	0.00116627	1.70545	0.00206285	-1.55238
16	NM_017437	0.00931561	1.55905	0.00962078	-1.55118
17	NM_001034173 /// NR_02775	0.00257108	2.11529	0.0118804	-1.55096
18	NM_018137	0.0056133	2.084	0.0236556	-1.54869
19	NM_005171	6.87E-05	2.10211	0.000337485	-1.54672
20	NM_001080541 /// NM_0011	0.00905335	1.53047	0.00844888	-1.5467
21	NM_022118	0.0157332	1.62151	0.0208901	-1.54554
22	NM_004774	0.0150562	1.76034	0.0303409	-1.5453
23	NM_001194954 /// NM_0011	0.00468483	2.0151	0.0178779	-1.54495
24	NM_005124	0.00608477	2.36448	0.0390852	-1.54415
25	NM_001267594 /// NM_0012	0.00137404	2.09255	0.00651288	-1.54098
26	NM_005746 /// NM_182790	0.0198042	1.56894	0.0221287	-1.54057
27	NM_025077	0.00251074	2.17736	0.0135262	-1.53949
28	NM_007018	0.00322467	2.18952	0.0174981	-1.53886
29	NM_053042	0.00340985	1.71443	0.00653773	-1.53731
30	NM_001042414 /// NR_00327	0.00583941	1.62296	0.00823651	-1.53593
31	NM_001029991 /// NM_0010	0.0141427	1.53537	0.0141223	-1.53572
32	NM_005387 /// NM_016320 /	0.00521122	2.3762	0.0358977	-1.53432
33	NM_001008860 /// NM_0010	0.00606597	2.48342	0.0464787	-1.5342
34	NM_017645	6.30E-05	1.55578	6.93E-05	-1.53418
35	NM_006510 /// NM_030950	5.12E-05	2.58906	0.000557933	-1.53327
36	NM_001007245 /// NM_0011	0.000265623	2.3617	0.00210355	-1.53321
37	NM_001135564 /// NM_0012	0.00149043	2.01742	0.00631119	-1.53294
38	NM_006275 /// NR_034009	0.00248658	2.58237	0.0236104	-1.53261
39	NM_001002926	0.0162128	1.82016	0.0395544	-1.5326
40	NM_001325	0.0133177	2.00652	0.0482491	-1.5322
41	NM_018394	0.00215987	2.62227	0.0217775	-1.53143
42	NM_007045 /// NM_194429	0.00145344	2.6646	0.0158825	-1.53031
43	NM_002936	0.00430173	1.63612	0.00655438	-1.52984
44	NM_207351	0.0088731	1.6194	0.012691	-1.5283
45	NM_001042482 /// NM_0224	0.00189085	2.62079	0.0195715	-1.52741
46	NM_004294	0.000117305	3.47015	0.00286971	-1.52677
47	NR_024510 /// NR_024511 //,	0.00537526	1.54171	0.00573942	-1.5267

1	NM_005614	0.00900041	2.14371	0.0436455	-1.52633
2	NM_004134	0.00263756	1.6808	0.00479532	-1.52588
3	NM_203448 /// NM_015363 //	0.00222292	2.8346	0.0281515	-1.52526
4	NM_001131035 /// NM_0011	0.00439763	1.53897	0.00468902	-1.52444
5	NM_018262 /// NM_052985 /	0.00811568	1.50966	0.00761447	-1.52387
6	NM_032146 /// NM_177976	0.000410802	5.15095	0.0207473	-1.52344
7	NM_001093755 /// NM_0010	0.00303905	2.92645	0.0403626	-1.52327
8	NM_022496 /// NR_048568 //	0.00193208	1.5153	0.00186756	-1.52265
9	XM_001128243	0.00821763	1.983	0.0311206	-1.52187
10	NM_182490	0.00205733	3.20374	0.0355332	-1.52179
11	NM_000201	0.000193245	5.24269	0.0107858	-1.52101
12	NM_001042399 /// NM_0161	0.00123215	1.83209	0.00362418	-1.52027
13	NM_001076683 /// NM_0010	0.000847391	2.00637	0.00376811	-1.52014
14	NM_001135608 /// NM_0150	0.00129219	3.40105	0.0270508	-1.52002
15	NM_018944	0.00690302	1.69472	0.0132329	-1.51959
16	NM_018944	0.013868	1.52903	0.0144487	-1.51946
17	NM_001205028 /// NM_0012	0.000806137	3.88096	0.0233597	-1.51896
18	NM_032505	0.000290064	2.78984	0.00410738	-1.51836
19	NM_013329 /// NM_016631 /	0.0035214	1.61198	0.00518583	-1.51829
20	NM_001159651 /// NM_1383	0.000973825	1.60086	0.00138723	-1.51802
21	NM_004586	0.00247377	1.69696	0.00493951	-1.51695
22	NM_020861	0.00233154	2.60135	0.024314	-1.51629
23	NM_001166356 /// NM_0011	0.000740403	1.82066	0.00216895	-1.51619
24	NM_001184906 /// NM_0328	0.0130097	1.73211	0.0276551	-1.51506
25	NR_029383	0.000949192	3.29063	0.019486	-1.5146
26	NM_052947	0.000163412	2.18989	0.00108344	-1.51437
27	NM_014188	0.0015565	1.89382	0.00546204	-1.51421
28	NM_030816	0.0215313	1.64863	0.0351374	-1.51391
29	NM_001159699 /// NM_0011	0.000348314	1.66204	0.000639741	-1.51304
30	NM_001001323 /// NM_0016	0.00233429	2.18538	0.0144113	-1.51166
31	NM_001191028 /// NM_0124	0.00378685	1.57763	0.00507527	-1.50975
32	NM_031923	0.00253032	2.31691	0.0191888	-1.50836
33	NM_001256182 /// NM_0012	0.00729822	1.60509	0.0109011	-1.50742
34	NM_017886	0.0246132	1.66862	0.0436872	-1.50629
35	NM_001099678	0.00323749	1.88534	0.0112836	-1.50612
36	NM_001185118 /// NM_0011	0.007014	1.71625	0.0152516	-1.50564
37	NM_001079516	0.00380819	2.6807	0.0426792	-1.50456
38	NM_017426	0.00232302	1.89509	0.00844907	-1.50448
39	NM_004990	0.000464368	2.13904	0.00290521	-1.50442
40	NM_001135608 /// NM_0150	0.00194909	2.71141	0.0243845	-1.50396
41	NM_001018089 /// NM_0246	0.0026262	2.09044	0.0141982	-1.50376
42	NM_001164665 /// NM_0209	0.00287405	1.89886	0.010594	-1.50175
43	NM_025138 /// NM_170719	0.00306428	1.67878	0.00617387	-1.50145
44	NM_001242826 /// NM_0057	0.00280012	2.11769	0.0160058	-1.50115
45	NM_001048249	0.00146558	1.54246	0.00177517	-1.50087
46	NM_004990	0.000991115	2.85147	0.01523	-1.5004
47	NM_001024647 /// NM_0224	0.00325009	2.08984	0.0176104	-1.50013

1
2 Supplementary Table 3 highly expressed genes in both xenograft FTSCt and HGSC (2 fold and p < 0.05, 2395)

5	Probeset ID	Gene Symbol	Gene Title
6	223278_at	GJB2	gap junction protein, beta 2, 26kDa
7	211719_x_at	FN1	fibronectin 1
8	207039_at	CDKN2A	cyclin-dependent kinase inhibitor 2A
9	225681_at	CTHRC1	collagen triple helix repeat containing 1
10	212464_s_at	FN1	fibronectin 1
11	216442_x_at	FN1	fibronectin 1
12	204268_at	S100A2	S100 calcium binding protein A2
13	210495_x_at	FN1	fibronectin 1
14	219918_s_at	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)
15	203186_s_at	S100A4	S100 calcium binding protein A4
16	228335_at	CLDN11	claudin 11
17	222608_s_at	ANLN	anillin, actin binding protein
18	201387_s_at	UCHL1	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)
19	208025_s_at	HMGA2	high mobility group AT-hook 2
20	209773_s_at	RRM2	ribonucleotide reductase M2
21	219148_at	PBK	PDZ binding kinase
22	202345_s_at	FABP5	fatty acid binding protein 5 (psoriasis-associated)
23	201645_at	TNC	tenascin C
24	218662_s_at	NCAPG	non-SMC condensin I complex, subunit G
25	203764_at	DLGAP5	discs, large (Drosophila) homolog-associated protein 5
26	204170_s_at	CKS2	CDC28 protein kinase regulatory subunit 2
27	204331_s_at	MRPS12	mitochondrial ribosomal protein S12
28	218585_s_at	DTL	denticleless E3 ubiquitin protein ligase homolog (Drosophila)
29	222958_s_at	DEPDC1	DEP domain containing 1
30	AFFX-HUMGAPDH/GAPDH /// GAPDH		glyceraldehyde-3-phosphate dehydrogenase /// glyceraldehyde-3
31	204822_at	TTK	TTK protein kinase
32	218663_at	NCAPG	non-SMC condensin I complex, subunit G
33	201890_at	RRM2	ribonucleotide reductase M2
34	201291_s_at	TOP2A	topoisomerase (DNA) II alpha 170kDa
35	210559_s_at	CDK1	cyclin-dependent kinase 1
36	236313_at	CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)
37	206445_s_at	PRMT1	protein arginine methyltransferase 1
38	201292_at	TOP2A	topoisomerase (DNA) II alpha 170kDa
39	202503_s_at	KIAA0101	KIAA0101
40	223490_s_at	EXOSC3	exosome component 3
41	209714_s_at	CDKN3	cyclin-dependent kinase inhibitor 3
42	228273_at	PRR11	proline rich 11
43	203554_x_at	PTTG1	pituitary tumor-transforming 1
44	211071_s_at	MLLT11	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog,
45	202870_s_at	CDC20	cell division cycle 20 homolog (S. cerevisiae)
46	219493_at	SHCBP1	SHC SH2-domain binding protein 1
47	202095_s_at	BIRC5	baculoviral IAP repeat containing 5
48	214710_s_at	CCNB1	cyclin B1

1	235545_at	DEPDC1	DEP domain containing 1
2	228053_s_at	TOMM5	translocase of outer mitochondrial membrane 5 homolog (yeast)
3	218542_at	CEP55	centrosomal protein 55kDa
4	218009_s_at	PRC1	protein regulator of cytokinesis 1
5	209642_at	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)
6	209644_x_at	CDKN2A	cyclin-dependent kinase inhibitor 2A
7	223381_at	NUF2	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)
8	224428_s_at	CDCA7	cell division cycle associated 7
9	222680_s_at	DTL	denticleless E3 ubiquitin protein ligase homolog (Drosophila)
10	203276_at	LMNB1	lamin B1
11	222037_at	MCM4	minichromosome maintenance complex component 4
12	218039_at	NUSAP1	nucleolar and spindle associated protein 1
13	219295_s_at	PCOLCE2	procollagen C-endopeptidase enhancer 2
14	207165_at	HMMR	hyaluronan-mediated motility receptor (RHAMM)
15	205046_at	CENPE	centromere protein E, 312kDa
16	206884_s_at	SCEL	scellin
17	223229_at	UBE2T	ubiquitin-conjugating enzyme E2T (putative)
18	218755_at	KIF20A	kinesin family member 20A
19	201105_at	LGALS1	lectin, galactoside-binding, soluble, 1
20	201505_at	LAMB1	laminin, beta 1
21	202954_at	UBE2C	ubiquitin-conjugating enzyme E2C
22	218883_s_at	MLF1IP	MLF1 interacting protein
23	214437_s_at	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)
24	203214_x_at	CDK1	cyclin-dependent kinase 1
25	209709_s_at	HMMR	hyaluronan-mediated motility receptor (RHAMM)
26	220651_s_at	MCM10	minichromosome maintenance complex component 10
27	208002_s_at	ACOT7	acyl-CoA thioesterase 7
28	207828_s_at	CENPF	centromere protein F, 350/400kDa (mitosin)
29	208079_s_at	AURKA	aurora kinase A
30	238756_at	GAS2L3	growth arrest-specific 2 like 3
31	209825_s_at	MIR3658 /// UCK2	microRNA 3658 /// uridine-cytidine kinase 2
32	203560_at	GGH	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl transferase)
33	229332_at	HPDL	4-hydroxyphenylpyruvate dioxygenase-like
34	204026_s_at	ZWINT	ZW10 interactor
35	213599_at	OIP5	Opa interacting protein 5
36	220295_x_at	DEPDC1	DEP domain containing 1
37	220083_x_at	UCHL5	ubiquitin carboxyl-terminal hydrolase L5
38	225655_at	UHRF1	ubiquitin-like with PHD and ring finger domains 1
39	225834_at	FAM72A /// FAM72B	/family with sequence similarity 72, member A /// family with sequence similarity 72, member B
40	205394_at	CHEK1	checkpoint kinase 1
41	204092_s_at	AURKA	aurora kinase A
42	203213_at	CDK1	cyclin-dependent kinase 1
43	225687_at	FAM83D	family with sequence similarity 83, member D
44	209679_s_at	SMAGP	small cell adhesion glycoprotein
45	239579_at	EPHX4	epoxide hydrolase 4
46	230165_at	SGOL2	shugoshin-like 2 (S. pombe)
47	206550_s_at	NUP155	nucleoporin 155kDa

1	201577_at	NME1	NME/NM23 nucleoside diphosphate kinase 1
2	213007_at	FANCI	Fanconi anemia, complementation group I
3	236641_at	KIF14	kinesin family member 14
4	201714_at	TUBG1	tubulin, gamma 1
5	226980_at	DEPDC1B	DEP domain containing 1B
6	213113_s_at	SLC43A3	solute carrier family 43, member 3
7	209900_s_at	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transpor
8	201663_s_at	SMC4	structural maintenance of chromosomes 4
9	218073_s_at	TMEM48	transmembrane protein 48
10	227928_at	PARPBP	PARP1 binding protein
11	221521_s_at	GINS2	GINS complex subunit 2 (Psf2 homolog)
12	202718_at	IGFBP2	insulin-like growth factor binding protein 2, 36kDa
13	204962_s_at	C2orf18 /// CENPA	chromosome 2 open reading frame 18 /// centromere protein A
14	209434_s_at	PPAT	phosphoribosyl pyrophosphate amidotransferase
15	218336_at	PFDN2	prefoldin subunit 2
16	222077_s_at	RACGAP1	Rac GTPase activating protein 1
17	202705_at	CCNB2	cyclin B2
18	205034_at	CCNE2	cyclin E2
19	203755_at	BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)
20	232231_at	RUNX2	runt-related transcription factor 2
21	204444_at	KIF11	kinesin family member 11
22	219979_s_at	C11orf73	chromosome 11 open reading frame 73
23	209891_at	SPC25	SPC25, NDC80 kinetochore complex component, homolog (S. cere
24	217755_at	HN1	hematological and neurological expressed 1
25	205129_at	NPM3	nucleophosmin/nucleoplasmin 3
26	204146_at	RAD51AP1	RAD51 associated protein 1
27	235609_at	BRIP1	BRCA1 interacting protein C-terminal helicase 1
28	210052_s_at	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)
29	202234_s_at	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transpor
30	232056_at	SCEL	scillin
31	221730_at	COL5A2	collagen, type V, alpha 2
32	219306_at	KIF15	kinesin family member 15
33	204709_s_at	KIF23	kinesin family member 23
34	222036_s_at	MCM4	minichromosome maintenance complex component 4
35	219555_s_at	CENPN	centromere protein N
36	226237_at	COL8A1	collagen, type VIII, alpha 1
37	228323_at	CASC5	cancer susceptibility candidate 5
38	204825_at	MELK	maternal embryonic leucine zipper kinase
39	228069_at	FAM54A	family with sequence similarity 54, member A
40	224870_at	DANCR	differentiation antagonizing non-protein coding RNA
41	201742_x_at	SRSF1	serine/arginine-rich splicing factor 1
42	205361_s_at	PFDN4	prefoldin subunit 4
43	235022_at	FAM210A	family with sequence similarity 210, member A
44	218252_at	CKAP2	cytoskeleton associated protein 2
45	225799_at	LINC00152 /// LOC541	long intergenic non-protein coding RNA 152 /// uncharacterized L
46	219410_at	TMEM45A	transmembrane protein 45A
47	213226_at	CCNA2	cyclin A2

1	1555772_a_at	CDC25A	cell division cycle 25 homolog A (S. pombe)
2	201202_at	PCNA	proliferating cell nuclear antigen
3	202206_at	ARL4C	ADP-ribosylation factor-like 4C
4	223570_at	MCM10	minichromosome maintenance complex component 10
5	227211_at	PHF19	PHD finger protein 19
6	1555225_at	C1orf43	chromosome 1 open reading frame 43
7	200634_at	PFN1	profilin 1
8	226661_at	CDCA2	cell division cycle associated 2
9	204887_s_at	PLK4	polo-like kinase 4
10	218726_at	HJURP	Holliday junction recognition protein
11	224913_s_at	TIMM50	translocase of inner mitochondrial membrane 50 homolog (S. cerevisiae)
12	218235_s_at	UTP11L	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)
13	1554572_a_at	SUV39H2	suppressor of variegation 3-9 homolog 2 (Drosophila)
14	224972_at	ROMO1	reactive oxygen species modulator 1
15	209796_s_at	CNPY2	canopy 2 homolog (zebrafish)
16	222443_s_at	RBM8A	RNA binding motif protein 8A
17	223403_s_at	POLR1B	polymerase (RNA) I polypeptide B, 128kDa
18	227212_s_at	PHF19	PHD finger protein 19
19	211981_at	COL4A1	collagen, type IV, alpha 1
20	220865_s_at	PDSS1	prenyl (decaprenyl) diphosphate synthase, subunit 1
21	212364_at	MYO1B	myosin IB
22	221987_s_at	TSR1	TSR1, 20S rRNA accumulation, homolog (S. cerevisiae)
23	207507_s_at	ATP5G3	ATP synthase, H ⁺ transporting, mitochondrial Fo complex, subunit I
24	223307_at	CDCA3	cell division cycle associated 3
25	202246_s_at	CDK4	cyclin-dependent kinase 4
26	213011_s_at	TPI1	triosephosphate isomerase 1
27	204836_at	GLDC	glycine dehydrogenase (decarboxylating)
28	206364_at	KIF14	kinesin family member 14
29	217728_at	S100A6	S100 calcium binding protein A6
30	212949_at	NCAPH	non-SMC condensin I complex, subunit H
31	202998_s_at	LOXL2	lysyl oxidase-like 2
32	226936_at	CENPW	centromere protein W
33	229551_x_at	ZNF367	zinc finger protein 367
34	222740_at	ATAD2	ATPase family, AAA domain containing 2
35	210466_s_at	SERBP1	SERPINE1 mRNA binding protein 1
36	222803_at	PRTFDC1	phosphoribosyl transferase domain containing 1
37	203022_at	RNASEH2A	ribonuclease H2, subunit A
38	218782_s_at	ATAD2	ATPase family, AAA domain containing 2
39	202613_at	CTPS1	CTP synthase 1
40	219978_s_at	NUSAP1	nucleolar and spindle associated protein 1
41	212094_at	PEG10	paternally expressed 10
42	223032_x_at	PRELID1	PRELI domain containing 1
43	214512_s_at	SUB1	SUB1 homolog (S. cerevisiae)
44	228977_at	LOC729680	uncharacterized LOC729680
45	201014_s_at	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole carboxylase
46	228729_at	CCNB1	cyclin B1
47	223556_at	HELLS	helicase, lymphoid-specific

1	212022_s_at	MKI67	antigen identified by monoclonal antibody Ki-67
2	221685_s_at	CCDC99	coiled-coil domain containing 99
3	210983_s_at	MCM7	minichromosome maintenance complex component 7
4	205909_at	POLE2	polymerase (DNA directed), epsilon 2, accessory subunit
5	208627_s_at	YBX1	Y box binding protein 1
6	206102_at	GINS1	GINS complex subunit 1 (Psf1 homolog)
7	225161_at	GFM1	G elongation factor, mitochondrial 1
8	203145_at	SPAG5	sperm associated antigen 5
9	225300_at	C15orf23	chromosome 15 open reading frame 23
10	206632_s_at	APOBEC3B	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like
11	201930_at	MCM6	minichromosome maintenance complex component 6
12	202635_s_at	POLR2K	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa
13	202094_at	BIRC5	baculoviral IAP repeat containing 5
14	209026_x_at	TUBB	tubulin, beta class I
15	201138_s_at	SSB	Sjogren syndrome antigen B (autoantigen La)
16	208767_s_at	LAPTM4B	lysosomal protein transmembrane 4 beta
17	204886_at	PLK4	polo-like kinase 4
18	209408_at	KIF2C	kinesin family member 2C
19	224345_x_at	FAM162A	family with sequence similarity 162, member A
20	202589_at	TYMS	thymidylate synthetase
21	208758_at	ATIC	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase
22	202207_at	ARL4C	ADP-ribosylation factor-like 4C
23	206074_s_at	HMGA1	high mobility group AT-hook 1
24	212782_x_at	POLR2J	polymerase (RNA) II (DNA directed) polypeptide J, 13.3kDa
25	204126_s_at	CDC45	cell division cycle 45 homolog (S. cerevisiae)
26	201478_s_at	DKC1 /// SNORA56	dyskeratosis congenita 1, dyskerin /// small nucleolar RNA, H/ACA
27	224637_at	OST4	oligosaccharyltransferase 4 homolog (S. cerevisiae)
28	200039_s_at	PSMB2	proteasome (prosome, macropain) subunit, beta type, 2
29	201072_s_at	SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of
30	201688_s_at	TPD52	tumor protein D52
31	224753_at	CDCA5	cell division cycle associated 5
32	211714_x_at	TUBB	tubulin, beta class I
33	217946_s_at	SAE1	SUMO1 activating enzyme subunit 1
34	212891_s_at	GADD45GIP1	growth arrest and DNA-damage-inducible, gamma interacting pro
35	212694_s_at	PCCB	propionyl CoA carboxylase, beta polypeptide
36	203931_s_at	MRPL12	mitochondrial ribosomal protein L12
37	223193_x_at	FAM162A	family with sequence similarity 162, member A
38	1554667_s_at	METTL8	methyltransferase like 8
39	208103_s_at	ANP32E	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E
40	221437_s_at	MRPS15	mitochondrial ribosomal protein S15
41	228597_at	MIS18A	MIS18 kinetochore protein homolog A (S. pombe)
42	202647_s_at	NRAS	neuroblastoma RAS viral (v-ras) oncogene homolog
43	208628_s_at	YBX1	Y box binding protein 1
44	204510_at	CDC7	cell division cycle 7 homolog (S. cerevisiae)
45	212563_at	BOP1	block of proliferation 1
46	200822_x_at	TPI1	triosephosphate isomerase 1
47	222883_at	SELRC1	Sel1 repeat containing 1

1	201725_at	CDC123	cell division cycle 123 homolog (<i>S. cerevisiae</i>)
2	225402_at	TP53RK	TP53 regulating kinase
3	201555_at	MCM3	minichromosome maintenance complex component 3
4	211519_s_at	KIF2C	kinesin family member 2C
5	209053_s_at	WHSC1	Wolf-Hirschhorn syndrome candidate 1
6	219787_s_at	ECT2	epithelial cell transforming sequence 2 oncogene
7	226545_at	CD109	CD109 molecule
8	200665_s_at	LOC100505813	/// SP/ uncharacterized LOC100505813 /// secreted protein, acidic, cyste
9	203046_s_at	TIMELESS	timeless homolog (<i>Drosophila</i>)
10	216228_s_at	WDHD1	WD repeat and HMG-box DNA binding protein 1
11	208967_s_at	AK2	adenylate kinase 2
12	200832_s_at	SCD	stearoyl-CoA desaturase (delta-9-desaturase)
13	205680_at	MMP10	matrix metallopeptidase 10 (stromelysin 2)
14	203358_s_at	EZH2	enhancer of zeste homolog 2 (<i>Drosophila</i>)
15	219000_s_at	DSCC1	defective in sister chromatid cohesion 1 homolog (<i>S. cerevisiae</i>)
16	226835_s_at	ZNFX1-AS1	ZNFX1 antisense RNA 1 (non-protein coding)
17	204023_at	RFC4	replication factor C (activator 1) 4, 37kDa
18	218605_at	TFB2M	transcription factor B2, mitochondrial
19	218027_at	MRPL15	mitochondrial ribosomal protein L15
20	203511_s_at	TRAPPC3	trafficking protein particle complex 3
21	201112_s_at	CSE1L	CSE1 chromosome segregation 1-like (yeast)
22	204127_at	RFC3	replication factor C (activator 1) 3, 38kDa
23	202309_at	MTHFD1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1
24	218512_at	WDR12	WD repeat domain 12
25	223774_at	SNHG12	/// SNORA16, small nucleolar RNA host gene 12 (non-protein coding) /// small n
26	222216_s_at	MRPL17	mitochondrial ribosomal protein L17
27	214431_at	GMPS	guanine monphosphate synthetase
28	211971_s_at	LRPPRC	leucine-rich pentatricopeptide repeat containing
29	226456_at	RMI2	RMI2, RecQ mediated genome instability 2, homolog (<i>S. cerevisiae</i>)
30	205436_s_at	H2AFX	H2A histone family, member X
31	224752_at	C7orf73	/// LOC10028 chromosome 7 open reading frame 73 /// chromosome 7 open re
32	221922_at	GPSM2	G-protein signaling modulator 2
33	217949_s_at	VKORC1	vitamin K epoxide reductase complex, subunit 1
34	218051_s_at	NT5DC2	5'-nucleotidase domain containing 2
35	203889_at	SCG5	secretogranin V (7B2 protein)
36	201689_s_at	TPD52	tumor protein D52
37	218355_at	KIF4A	kinesin family member 4A
38	223993_s_at	CNIH4	cornichon homolog 4 (<i>Drosophila</i>)
39	202856_s_at	SLC16A3	solute carrier family 16, member 3 (monocarboxylic acid transpor
40	202690_s_at	SNRPD1	small nuclear ribonucleoprotein D1 polypeptide 16kDa
41	225099_at	FBXO45	F-box protein 45
42	238075_at	CHEK1	checkpoint kinase 1
43	222701_s_at	CHCHD7	coiled-coil-helix-coiled-coil-helix domain containing 7
44	212320_at	TUBB	tubulin, beta class I
45	228559_at	CENPN	centromere protein N
46	212013_at	PXDN	peroxidasin homolog (<i>Drosophila</i>)
47	224217_s_at	FAF1	Fas (TNFRSF6) associated factor 1

1			
2	202580_x_at	FOXM1	forkhead box M1
3	201629_s_at	ACP1	acid phosphatase 1, soluble
4	223062_s_at	PSAT1	phosphoserine aminotransferase 1
5	201096_s_at	ARF4	ADP-ribosylation factor 4
6	201897_s_at	CKS1B	CDC28 protein kinase regulatory subunit 1B
7	225827_at	EIF2C2	eukaryotic translation initiation factor 2C, 2
8	227350_at	HELLS	helicase, lymphoid-specific
9	208581_x_at	MT1X	metallothionein 1X
10	224523_s_at	C3orf26	chromosome 3 open reading frame 26
11	239002_at	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)
12	231855_at	KIAA1524	KIAA1524
13	235425_at	SGOL2	shugoshin-like 2 (S. pombe)
14	222039_at	KIF18B	kinesin family member 18B
15	213133_s_at	GCSH	glycine cleavage system protein H (aminomethyl carrier)
16	229442_at	C18orf54	chromosome 18 open reading frame 54
17	204165_at	WASF1	WAS protein family, member 1
18	224320_s_at	MCM8	minichromosome maintenance complex component 8
19	203119_at	CCDC86	coiled-coil domain containing 86
20	213427_at	RPP40	ribonuclease P/MRP 40kDa subunit
21	218586_at	C20orf20	chromosome 20 open reading frame 20
22	205024_s_at	RAD51	RAD51 homolog (S. cerevisiae)
23	212141_at	MCM4	minichromosome maintenance complex component 4
24	1555878_at	RPS24	Ribosomal protein S24
25	207508_at	ATP5G3	ATP synthase, H ⁺ transporting, mitochondrial Fo complex, subunit 1
26	218695_at	EXOSC4	exosome component 4
27	203270_at	DTYMK	deoxythymidylate kinase (thymidylate kinase)
28	225943_at	NLN	neurolysin (metallopeptidase M3 family)
29	202591_s_at	MIR5096 /// SSBP1	microRNA 5096 /// single-stranded DNA binding protein 1, mitochondrial
30	229305_at	MLF1IP	MLF1 interacting protein
31	202296_s_at	RER1	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)
32	221520_s_at	CDCA8	cell division cycle associated 8
33	204641_at	NEK2	NIMA (never in mitosis gene a)-related kinase 2
34	1553984_s_at	DTYMK	deoxythymidylate kinase (thymidylate kinase)
35	228868_x_at	CDT1	Chromatin licensing and DNA replication factor 1
36	228564_at	LOC375295	uncharacterized LOC375295
37	200975_at	PPT1	palmitoyl-protein thioesterase 1
38	201848_s_at	BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3
39	201263_at	TARS	threonyl-tRNA synthetase
40	212458_at	SPRED2	sprouty-related, EVH1 domain containing 2
41	222843_at	FIGNL1	fidgetin-like 1
42	204695_at	CDC25A	cell division cycle 25 homolog A (S. pombe)
43	201231_s_at	ENO1	enolase 1, (alpha)
44	205402_x_at	PRSS2	protease, serine, 2 (trypsin 2)
45	212789_at	NCAPD3	non-SMC condensin II complex, subunit D3
46	211762_s_at	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
47	216470_x_at	PRSS2	protease, serine, 2 (trypsin 2)
48	200658_s_at	PHB	prohibitin

1	227942_s_at	CRIP	cysteine-rich PDZ-binding protein
2	220011_at	C1orf135	chromosome 1 open reading frame 135
3	228931_at	COQ4	coenzyme Q4 homolog (S. cerevisiae)
4	223480_s_at	MRPL47	mitochondrial ribosomal protein L47
5	219544_at	BORA	bora, aurora kinase A activator
6	204610_s_at	CCDC85B	coiled-coil domain containing 85B
7	221692_s_at	MRPL34	mitochondrial ribosomal protein L34
8	205499_at	SRPX2	sushi-repeat containing protein, X-linked 2
9	238996_x_at	ALDOA	aldolase A, fructose-bisphosphate
10	223055_s_at	XPO5	exportin 5
11	202666_s_at	ACTL6A	actin-like 6A
12	205167_s_at	CDC25C	cell division cycle 25 homolog C (S. pombe)
13	225439_at	NUDCD1	NudC domain containing 1
14	213008_at	FANCI	Fanconi anemia, complementation group I
15	AFFX-HUMGAPDH/GAPDH /// GAPDH		glyceraldehyde-3-phosphate dehydrogenase /// glyceraldehyde-3
16	224714_at	MKI67IP	MKI67 (FHA domain) interacting nucleolar phosphoprotein
17	203625_x_at	SKP2	S-phase kinase-associated protein 2, E3 ubiquitin protein ligase
18	212680_x_at	PPP1R14B	protein phosphatase 1, regulatory (inhibitor) subunit 14B
19	204162_at	NDC80	NDC80 kinetochore complex component homolog (S. cerevisiae)
20	202310_s_at	COL1A1	collagen, type I, alpha 1
21	203818_s_at	SF3A3	splicing factor 3a, subunit 3, 60kDa
22	225853_at	GNPNAT1	glucosamine-phosphate N-acetyltransferase 1
23	212816_s_at	CBS	cystathionine-beta-synthase
24	205122_at	MSANTD3-TMEFF1 /// MSANTD3-TMEFF1	readthrough /// transmembrane protein with
25	228468_at	MASTL	microtubule associated serine/threonine kinase-like
26	205733_at	BLM	Bloom syndrome, RecQ helicase-like
27	214095_at	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)
28	200744_s_at	GNB1	guanine nucleotide binding protein (G protein), beta polypeptide
29	201664_at	SMC4	structural maintenance of chromosomes 4
30	224376_s_at	C20orf24 /// TGIF2-C2	chromosome 20 open reading frame 24 /// TGIF2-C20orf24 readt
31	213647_at	DNA2	DNA replication helicase 2 homolog (yeast)
32	219311_at	CEP76	centrosomal protein 76kDa
33	211980_at	COL4A1	collagen, type IV, alpha 1
34	200925_at	COX6A1	cytochrome c oxidase subunit VIa polypeptide 1
35	226943_at	C12orf73	chromosome 12 open reading frame 73
36	227477_at	ZMYND19	zinc finger, MYND-type containing 19
37	202107_s_at	MCM2	minichromosome maintenance complex component 2
38	218984_at	PUS7	pseudouridylate synthase 7 homolog (S. cerevisiae)
39	209781_s_at	KHDRBS3	KH domain containing, RNA binding, signal transduction associate
40	229742_at	C15orf61	chromosome 15 open reading frame 61
41	208875_s_at	PAK2	p21 protein (Cdc42/Rac)-activated kinase 2
42	224232_s_at	PRELID1	PRELI domain containing 1
43	224331_s_at	MRPL36	mitochondrial ribosomal protein L36
44	218187_s_at	C8orf33	chromosome 8 open reading frame 33
45	202839_s_at	NDUFB7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa
46	202806_at	DBN1	drebrin 1
47	205449_at	SAC3D1	SAC3 domain containing 1

1	204584_at	L1CAM	L1 cell adhesion molecule
2	225036_at	TOMM5	translocase of outer mitochondrial membrane 5 homolog (yeast)
3	203417_at	MFAP2	microfibrillar-associated protein 2
4	222702_x_at	CRIP1	cysteine-rich PDZ-binding protein
5	236075_s_at	LOC100506676	uncharacterized LOC100506676
6	212296_at	PSMD14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14
7	201564_s_at	FSCN1 /// LOC100653	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)
8	227165_at	SKA3	spindle and kinetochore associated complex subunit 3
9	229097_at	DIAPH3	diaphanous homolog 3 (Drosophila)
10	221676_s_at	CORO1C	coronin, actin binding protein, 1C
11	220060_s_at	PARPBP	PARP1 binding protein
12	232238_at	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)
13	202667_s_at	SLC39A7	solute carrier family 39 (zinc transporter), member 7
14	201774_s_at	NCAPD2	non-SMC condensin I complex, subunit D2
15	211456_x_at	MT1P2	metallothionein 1 pseudogene 2
16	202715_at	CAD	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, cytosolic
17	218479_s_at	XPO4	exportin 4
18	223020_at	CLPTM1L	CLPTM1-like
19	223839_s_at	SCD	stearoyl-CoA desaturase (delta-9-desaturase)
20	203347_s_at	MTF2	metal response element binding transcription factor 2
21	217829_s_at	USP39	ubiquitin specific peptidase 39
22	223413_s_at	LYAR	Ly1 antibody reactive homolog (mouse)
23	211318_s_at	RAE1	RAE1 RNA export 1 homolog (S. pombe)
24	1558750_a_at	LOC100288637	OTU domain containing 7A pseudogene
25	225291_at	PNPT1	polyribonucleotide nucleotidyltransferase 1
26	217398_x_at	GAPDH	glyceraldehyde-3-phosphate dehydrogenase
27	203577_at	GTF2H4	general transcription factor IIH, polypeptide 4, 52kDa
28	202016_at	MEST	mesoderm specific transcript homolog (mouse)
29	234464_s_at	EME1	essential meiotic endonuclease 1 homolog 1 (S. pombe)
30	213088_s_at	DNAJC9	DnaJ (Hsp40) homolog, subfamily C, member 9
31	204033_at	TRIP13	thyroid hormone receptor interactor 13
32	223461_at	TBC1D7	TBC1 domain family, member 7
33	221436_s_at	CDCA3	cell division cycle associated 3
34	220094_s_at	CCDC90A	coiled-coil domain containing 90A
35	200770_s_at	LAMC1	laminin, gamma 1 (formerly LAMB2)
36	202311_s_at	COL1A1	collagen, type I, alpha 1
37	218982_s_at	MRPS17	mitochondrial ribosomal protein S17
38	228281_at	C11orf82	chromosome 11 open reading frame 82
39	201672_s_at	USP14	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)
40	222497_x_at	NMD3	NMD3 homolog (S. cerevisiae)
41	221845_s_at	CLPB	ClpB caseinolytic peptidase B homolog (E. coli)
42	225788_at	RRP36	ribosomal RNA processing 36 homolog (S. cerevisiae)
43	218193_s_at	GOLT1B	golgi transport 1B
44	204724_s_at	COL9A3	collagen, type IX, alpha 3
45	218080_x_at	FAF1	Fas (TNFRSF6) associated factor 1
46	229886_at	C5orf34	chromosome 5 open reading frame 34
47	225593_at	LSM10	LSM10, U7 small nuclear RNA associated

1	200657_at	SLC25A5	solute carrier family 25 (mitochondrial carrier; adenine nucleotide
2	200910_at	CCT3	chaperonin containing TCP1, subunit 3 (gamma)
3	202706_s_at	UMPS	uridine monophosphate synthetase
4	205339_at	STIL	SCL/TAL1 interrupting locus
5	204728_s_at	WDHD1	WD repeat and HMG-box DNA binding protein 1
6	228990_at	SNHG12 /// SNORA16	small nucleolar RNA host gene 12 (non-protein coding) /// small n
7	200966_x_at	ALDOA	aldolase A, fructose-bisphosphate
8	224623_at	LOC728554	/// THOC3 THO complex 3 pseudogene /// THO complex 3
9	218399_s_at	CDCA4	cell division cycle associated 4
10	201074_at	SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of
11	201417_at	SOX4	SRY (sex determining region Y)-box 4
12	1554101_a_at	TMTC4	transmembrane and tetratricopeptide repeat containing 4
13	220789_s_at	SNORA5B /// TBRG4	small nucleolar RNA, H/ACA box 5B /// transforming growth facto
14	218308_at	TACC3	transforming, acidic coiled-coil containing protein 3
15	223880_x_at	C20orf24 /// TGIF2-C2	chromosome 20 open reading frame 24 /// TGIF2-C20orf24 readtl
16	206461_x_at	MT1H	metallothionein 1H
17	232065_x_at	CENPL	centromere protein L
18	241937_s_at	WDR4	WD repeat domain 4
19	204957_at	ORC5	origin recognition complex, subunit 5
20	211576_s_at	SLC19A1	solute carrier family 19 (folate transporter), member 1
21	222714_s_at	LACTB2	lactamase, beta 2
22	210766_s_at	CSE1L	CSE1 chromosome segregation 1-like (yeast)
23	211594_s_at	MRPL9	mitochondrial ribosomal protein L9
24	213523_at	CCNE1	cyclin E1
25	203502_at	BPGM	2,3-bisphosphoglycerate mutase
26	235509_at	LOC100506538	/// ND uncharacterized LOC100506538 /// NADH dehydrogenase (ubiqui
27	210976_s_at	PFKM	phosphofructokinase, muscle
28	219510_at	POLQ	polymerase (DNA directed), theta
29	228733_at	PUSL1	pseudouridylate synthase-like 1
30	216237_s_at	MCM5	minichromosome maintenance complex component 5
31	204853_at	ORC2	origin recognition complex, subunit 2
32	217834_s_at	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein
33	58696_at	EXOSC4	exosome component 4
34	1568873_at	ZNF519	zinc finger protein 519
35	235704_at	DAZAP2	DAZ associated protein 2
36	220607_x_at	TH1L	TH1-like (Drosophila)
37	225693_s_at	CAMTA1	calmodulin binding transcription activator 1
38	230954_at	C20orf112	chromosome 20 open reading frame 112
39	216222_s_at	MYO10	myosin X
40	200644_at	MARCKSL1	MARCKS-like 1
41	208308_s_at	GPI	glucose-6-phosphate isomerase
42	219420_s_at	SELRC1	Sel1 repeat containing 1
43	225657_at	LOC152217	uncharacterized LOC152217
44	225638_at	C1orf31	chromosome 1 open reading frame 31
45	201322_at	ATP5B	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, beta pol
46	210933_s_at	FSCN1 /// LOC100653	fascin homolog 1, actin-bundling protein (Strongylocentrotus purp
47	200818_at	ATP5O	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, O subu

1	227896_at	BCCIP	BRCA2 and CDKN1A interacting protein
2	201757_at	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-solute carrier family 38, member 1
3	224579_at	SLC38A1	processing of precursor 7, ribonuclease P/MRP subunit (S. cerevisiae) junctophilin 1
4	209482_at	POP7	myosin X
5	229139_at	JPH1	RAD21 homolog (S. pombe)
6	201976_s_at	MYO10	transmembrane protein 237
7	200607_s_at	RAD21	metallothionein 1F
8	1553956_at	TMEM237	aldolase A, fructose-bisphosphate
9	217165_x_at	MT1F	atlakin GTPase 3
10	214687_x_at	ALDOA	S100 calcium binding protein A13
11	223452_s_at	ATL3	poly (ADP-ribose) polymerase 2
12	202598_at	S100A13	flap structure-specific endonuclease 1
13	214086_s_at	PARP2	origin recognition complex, subunit 6
14	204767_s_at	FEN1	BRCA1 associated RING domain 1
15	219105_x_at	ORC6	antigen identified by monoclonal antibody Ki-67
16	227545_at	BARD1	KRI1 homolog (S. cerevisiae)
17	212023_s_at	MKI67	chromosome 19 open reading frame 48
18	227587_at	KRI1	translocase of outer mitochondrial membrane 40 homolog (yeast)
19	224468_s_at	C19orf48	coiled-coil domain containing 137
20	226059_at	TOMM40L	melanoma cell adhesion molecule
21	225933_at	CCDC137	TH1-like (Drosophila)
22	211042_x_at	MCAM	cleavage stimulation factor, 3' pre-RNA, subunit 1, 50kDa
23	225261_x_at	TH1L	glyceraldehyde-3-phosphate dehydrogenase
24	202190_at	CSTF1	aurora kinase A interacting protein 1
25	213453_x_at	GAPDH	sorting nexin 5
26	218580_x_at	AURKAIP1	centromere protein F, 350/400kDa (mitosin)
27	222417_s_at	SNX5	Niemann-Pick disease, type C1
28	209172_s_at	CENPF	G-2 and S-phase expressed 1
29	202679_at	NPC1	large subunit GTPase 1 homolog (S. cerevisiae)
30	204315_s_at	GTSE1	zinc finger protein 518B
31	221535_at	LSG1	RAB7A, member RAS oncogene family
32	226909_at	ZNF518B	centrosomal protein 76kDa
33	211960_s_at	RAB7A	stathmin 1
34	52285_f_at	CEP76	arginine/serine-rich coiled-coil 1
35	200783_s_at	STMN1	COMM domain containing 2
36	1555501_s_at	RSRC1	bola homolog 2 (E. coli) /// bola homolog 2B (E. coli)
37	223491_at	COMM2	glyceraldehyde-3-phosphate dehydrogenase
38	209836_x_at	BOLA2 /// BOLA2B	asparaginyl-tRNA synthetase 2, mitochondrial (putative)
39	212581_x_at	GAPDH	PET100 homolog (S. cerevisiae)
40	219217_at	NARS2	mitochondrial ribosomal protein S15
41	226006_at	PET100	ubiquilin 1
42	226296_s_at	MRPS15	protein phosphatase 1, catalytic subunit, alpha isozyme
43	222989_s_at	UBQLN1	RAD1 homolog (S. pombe)
44	200846_s_at	PPP1CA	phosphoglycolate phosphatase
45	235253_at	RAD1	discs, large homolog 1 (Drosophila)
46	222622_at	PGP	
47	202514_at	DLG1	

1	225100_at	FBXO45	F-box protein 45
2	213175_s_at	SNRPB	small nuclear ribonucleoprotein polypeptides B and B1
3	209609_s_at	MRPL9	mitochondrial ribosomal protein L9
4	208962_s_at	FADS1 /// MIR1908	fatty acid desaturase 1 /// microRNA 1908
5	201818_at	LPCAT1	lysophosphatidylcholine acyltransferase 1
6	233588_x_at	PFDN6	prefoldin subunit 6
7	203039_s_at	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-)
8	222593_s_at	SPATS2	spermatogenesis associated, serine-rich 2
9	225401_at	C1orf85	chromosome 1 open reading frame 85
10	213787_s_at	EBP	emopamil binding protein (sterol isomerase)
11	206316_s_at	KNTC1	kinetochore associated 1
12	221522_at	ANKRD27	ankyrin repeat domain 27 (VPS9 domain)
13	223234_at	MAD2L2	MAD2 mitotic arrest deficient-like 2 (yeast)
14	225841_at	HENMT1	HEN1 methyltransferase homolog 1 (Arabidopsis)
15	220642_x_at	GPR89A /// GPR89B // G protein-coupled receptor 89A // G protein-coupled receptor 89B	G protein-coupled receptor 89A // G protein-coupled receptor 89B
16	203209_at	RFC5	replication factor C (activator 1) 5, 36.5kDa
17	202183_s_at	KIF22	kinesin family member 22
18	222700_at	ATL2	atlastin GTPase 2
19	223231_at	TATDN1	TatD DNase domain containing 1
20	204326_x_at	MT1X	metallothionein 1X
21	218712_at	C1orf109	chromosome 1 open reading frame 109
22	201896_s_at	PSRC1	proline-serine-rich coiled-coil 1
23	204700_x_at	DIEXF	digestive organ expansion factor homolog (zebrafish)
24	200075_s_at	GUK1	guanylate kinase 1
25	235572_at	SPC24	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)
26	224521_s_at	CCDC77	coiled-coil domain containing 77
27	204173_at	MYL6B	myosin, light chain 6B, alkali, smooth muscle and non-muscle
28	227517_s_at	GAS5 /// SNORD44 /// growth arrest-specific 5 (non-protein coding) // small nucleolar RNA	extra spindle pole bodies homolog 1 (S. cerevisiae)
29	38158_at	ESPL1	drebrin 1
30	217025_s_at	DBN1	proteasome (prosome, macropain) subunit, alpha type, 7
31	216088_s_at	PSMA7	ring finger protein 7
32	224439_x_at	RNF7	fatty acid desaturase 1 /// microRNA 1908
33	208964_s_at	UMPS	uridine monophosphate synthetase
34	215165_x_at	LSM4	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)
35	202737_s_at	SPIRE1	spire homolog 1 (Drosophila)
36	225018_at	CNPY2	canopy 2 homolog (zebrafish)
37	202857_at	GNAI3	guanine nucleotide binding protein (G protein), alpha inhibiting ac
38	201180_s_at	AURKAIP1	aurora kinase A interacting protein 1
39	225552_x_at	CEP152	centrosomal protein 152kDa
40	239413_at	ZBTB8OS	zinc finger and BTB domain containing 8 opposite strand
41	228970_at	UNG	uracil-DNA glycosylase
42	202330_s_at	CDC25B	cell division cycle 25 homolog B (S. pombe)
43	201853_s_at	RAB10	RAB10, member RAS oncogene family
44	222981_s_at	PFDN6	prefoldin subunit 6
45	222029_x_at	TOR1AIP2	torsin A interacting protein 2
46	225880_at	KIAA0317	KIAA0317

1			
2	201790_s_at	DHCR7	7-dehydrocholesterol reductase
3	212654_at	TPM2	tropomyosin 2 (beta)
4	201584_s_at	DDX39A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39A
5	230060_at	CDCA7	cell division cycle associated 7
6	1554390_s_at	ACTR2	ARP2 actin-related protein 2 homolog (yeast)
7	235463_s_at	CERS6	ceramide synthase 6
8	221538_s_at	PLXNA1	plexin A1
9	204558_at	RAD54L	RAD54-like (<i>S. cerevisiae</i>)
10	217943_s_at	MAP7D1	MAP7 domain containing 1
11	203190_at	MIR4691 /// NDUFS8	microRNA 4691 /// NADH dehydrogenase (ubiquinone) Fe-S protein
12	203105_s_at	DNM1L	dynamin 1-like
13	1555764_s_at	TIMM10	translocase of inner mitochondrial membrane 10 homolog (yeast)
14	204752_x_at	PARP2	poly (ADP-ribose) polymerase 2
15	215227_x_at	ACP1	acid phosphatase 1, soluble
16	213334_x_at	HAUS7	HAUS augmin-like complex, subunit 7
17	206032_at	DSC3	desmocollin 3
18	203234_at	UPP1	uridine phosphorylase 1
19	202824_s_at	TCEB1	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongating)
20	201970_s_at	NASP	nuclear autoantigenic sperm protein (histone-binding)
21	212165_at	TMEM183A /// TMEM	transmembrane protein 183A /// transmembrane protein 183B
22	222992_s_at	NDUFB9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa
23	201587_s_at	IRAK1	interleukin-1 receptor-associated kinase 1
24	219402_s_at	DERL1	derlin 1
25	223524_s_at	TMEM108	transmembrane protein 108
26	234311_s_at	GTPBP10	GTP-binding protein 10 (putative)
27	200980_s_at	PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1
28	201433_s_at	PTDSS1	phosphatidylserine synthase 1
29	238964_at	FIGN	fidgetin
30	228245_s_at	LOC100509445 /// LOC100509445	uncharacterized LOC100509445 /// ovostatin homolog 2-like /// c
31	208941_s_at	SEPHS1	selenophosphate synthetase 1
32	225006_x_at	TH1L	TH1-like (<i>Drosophila</i>)
33	218286_s_at	RNF7	ring finger protein 7
34	217733_s_at	TMSB10	thymosin beta 10
35	203228_at	PAFAH1B3	platelet-activating factor acetylhydrolase 1b, catalytic subunit 3 (2)
36	226473_at	CBX2	chromobox homolog 2
37	202961_s_at	ATP5J2	ATP synthase, H ⁺ transporting, mitochondrial Fo complex, subunit 2
38	209744_x_at	ITCH	itchy E3 ubiquitin protein ligase
39	224932_at	CHCHD10	coiled-coil-helix-coiled-coil-helix domain containing 10
40	221711_s_at	BABAM1	BRISC and BRCA1 A complex member 1
41	213843_x_at	SLC6A8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8
42	235266_at	ATAD2	ATPase family, AAA domain containing 2
43	221909_at	RNFT2	ring finger protein, transmembrane 2
44	201114_x_at	PSMA7	proteasome (prosome, macropain) subunit, alpha type, 7
45	214096_s_at	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)
46	210115_at	RPL39L	ribosomal protein L39-like
47	209680_s_at	KIFC1	kinesin family member C1
48	201390_s_at	CSNK2B	casein kinase 2, beta polypeptide

1	209882_at	RIT1	Ras-like without CAAX 1
2	226616_s_at	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa
3	226947_at	GUSBP1 /// GUSBP4	glucuronidase, beta pseudogene 1 /// glucuronidase, beta pseudogene 4
4	204839_at	POP5	processing of precursor 5, ribonuclease P/MRP subunit (S. cerevisiae)
5	204745_x_at	MT1G	metallothionein 1G
6	201064_s_at	PABPC4	poly(A) binding protein, cytoplasmic 4 (inducible form)
7	225317_at	ACBD6	acyl-CoA binding domain containing 6
8	210854_x_at	SLC6A8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8
9	218590_at	C10orf2	chromosome 10 open reading frame 2
10	239710_at	FIGN	fidgetin
11	202633_at	TOPBP1	topoisomerase (DNA) II binding protein 1
12	227455_at	C6orf136	chromosome 6 open reading frame 136
13	213906_at	MYBL1	v-myb myeloblastosis viral oncogene homolog (avian)-like 1
14	222894_x_at	NDUFAF5	NADH dehydrogenase (ubiquinone) complex I, assembly factor 5
15	201441_at	COX6B1	cytochrome c oxidase subunit VIb polypeptide 1 (ubiquitous)
16	206261_at	ZNF239	zinc finger protein 239
17	201379_s_at	TPD52L2	tumor protein D52-like 2
18	226161_at	SLC30A6	solute carrier family 30 (zinc transporter), member 6
19	201727_s_at	ELAVL1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen)
20	235694_at	TCFL5	transcription factor-like 5 (basic helix-loop-helix)
21	221591_s_at	FAM64A	family with sequence similarity 64, member A
22	222640_at	DNMT3A	DNA (cytosine-5-)methyltransferase 3 alpha
23	228049_x_at	LOC100507303	uncharacterized LOC100507303
24	203025_at	NAA10	N(alpha)-acetyltransferase 10, NatA catalytic subunit
25	210213_s_at	EIF6	eukaryotic translation initiation factor 6
26	225865_x_at	TH1L	TH1-like (Drosophila)
27	201310_s_at	NREP	neuronal regeneration related protein homolog (rat)
28	223374_s_at	B3GALNT1	beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group antigen)
29	222763_s_at	SFT2D3 /// WDR33	SFT2 domain containing 3 /// WD repeat domain 33
30	223244_s_at	NDUFA12	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12
31	202279_at	C14orf2	chromosome 14 open reading frame 2
32	204228_at	PPIH	peptidylprolyl isomerase H (cyclophilin H)
33	204256_at	ELOVL6	ELOVL fatty acid elongase 6
34	200625_s_at	CAP1	CAP, adenylate cyclase-associated protein 1 (yeast)
35	209015_s_at	DNAJB6	DnaJ (Hsp40) homolog, subfamily B, member 6
36	1555241_at	C8orf59	chromosome 8 open reading frame 59
37	225427_s_at	APOA1BP	apolipoprotein A-I binding protein
38	226452_at	PDK1	pyruvate dehydrogenase kinase, isozyme 1
39	218408_at	TIMM10	translocase of inner mitochondrial membrane 10 homolog (yeast)
40	209589_s_at	EPHB2	EPH receptor B2
41	208029_s_at	LAPTM4B	lysosomal protein transmembrane 4 beta
42	212175_s_at	AK2	adenylate kinase 2
43	218770_s_at	TMEM39B	transmembrane protein 39B
44	212791_at	C1orf216	chromosome 1 open reading frame 216
45	202059_s_at	KPNA1	karyopherin alpha 1 (importin alpha 5)
46	201091_s_at	CBX3	chromobox homolog 3
47	204348_s_at	AK4 /// LOC100507851	adenylate kinase 4 /// adenylate kinase isoenzyme 4, mitochondrial

1	212058_at	U2SURP	U2 snRNP-associated SURP domain containing
2	212411_at	IMP4	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)
3	216026_s_at	POLE	polymerase (DNA directed), epsilon, catalytic subunit
4	208795_s_at	MCM7	minichromosome maintenance complex component 7
5	204817_at	ESPL1	extra spindle pole bodies homolog 1 (<i>S. cerevisiae</i>)
6	235029_at	GINS4	GINS complex subunit 4 (Sld5 homolog)
7	227852_at	RP9	retinitis pigmentosa 9 (autosomal dominant)
8	207714_s_at	SERPINH1	serpin peptidase inhibitor, clade H (heat shock protein 47), memb
9	222606_at	ZWILCH	Zwilch, kinetochore associated, homolog (<i>Drosophila</i>)
10	219119_at	NAA38	N(alpha)-acetyltransferase 38, NatC auxiliary subunit
11	208698_s_at	NONO	non-POU domain containing, octamer-binding
12	208743_s_at	YWHA _B	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activat
13	221962_s_at	UBE2H	ubiquitin-conjugating enzyme E2H
14	225963_at	KLHDC5	kelch domain containing 5
15	223024_at	AP1M1	adaptor-related protein complex 1, mu 1 subunit
16	204766_s_at	NUDT1	nudix (nucleoside diphosphate linked moiety X)-type motif 1
17	218897_at	TMEM177	transmembrane protein 177
18	218481_at	EXOSC5	exosome component 5
19	200771_at	LAMC1	laminin, gamma 1 (formerly LAMB2)
20	220864_s_at	NDUFA13	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13
21	40148_at	APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2
22	217835_x_at	C20orf24 /// TGIF2-C2	chromosome 20 open reading frame 24 /// TGIF2-C20orf24 readtl
23	229666_s_at	CSTF3	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa
24	224578_at	RCC2	regulator of chromosome condensation 2
25	204668_at	RNF24	ring finger protein 24
26	201770_at	SNRPA	small nuclear ribonucleoprotein polypeptide A
27	214005_at	GGCX	gamma-glutamyl carboxylase
28	223560_s_at	C2orf56	chromosome 2 open reading frame 56
29	202475_at	TMEM147	transmembrane protein 147
30	1558692_at	C1orf85	chromosome 1 open reading frame 85
31	228252_at	PIF1	PIF1 5'-to-3' DNA helicase homolog (<i>S. cerevisiae</i>)
32	200692_s_at	HSPA9	heat shock 70kDa protein 9 (mortalin)
33	220942_x_at	FAM162A	family with sequence similarity 162, member A
34	219522_at	FJX1	four jointed box 1 (<i>Drosophila</i>)
35	1557945_at	TCTE3	T-complex-associated-testis-expressed 3
36	232398_at	CCDC150	coiled-coil domain containing 150
37	208821_at	SNRPB	small nuclear ribonucleoprotein polypeptides B and B1
38	200862_at	DHCR24	24-dehydrocholesterol reductase
39	220223_at	ATAD5	ATPase family, AAA domain containing 5
40	218507_at	HILPDA	hypoxia inducible lipid droplet-associated
41	1553972_a_at	CBS	cystathionine-beta-synthase
42	202219_at	SLC6A8	solute carrier family 6 (neurotransmitter transporter, creatine), m
43	212621_at	TMEM194A	transmembrane protein 194A
44	236718_at	MYO10	myosin X
45	203736_s_at	PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1)
46	223690_at	LTBP2	latent transforming growth factor beta binding protein 2
47	200608_s_at	RAD21	RAD21 homolog (<i>S. pombe</i>)

1	209104_s_at	NHP2	NHP2 ribonucleoprotein homolog (yeast)
2	213696_s_at	MED8	mediator complex subunit 8
3	214804_at	CENPI	centromere protein I
4	234926_s_at	C20orf43	chromosome 20 open reading frame 43
5	228671_at	TMEM201	transmembrane protein 201
6	212877_at	KLC1	kinesin light chain 1
7	228401_at	ATAD2	ATPase family, AAA domain containing 2
8	201111_at	CSE1L	CSE1 chromosome segregation 1-like (yeast)
9	215812_s_at	LOC653562 /// SLC6A1	sodium- and chloride-dependent creatine transporter 1-like /// sodium- and chloride-dependent creatine transporter 1-like (yeast)
10	227997_at	IL17RD	interleukin 17 receptor D
11	231517_at	ZYG11A	zyg-11 homolog A (C. elegans)
12	1554020_at	BICD1	bicaudal D homolog 1 (Drosophila)
13	222514_at	RRAGC	Ras-related GTP binding C
14	213671_s_at	MARS	methionyl-tRNA synthetase
15	225991_at	TMEM41A	transmembrane protein 41A
16	201264_at	COPE	coatomer protein complex, subunit epsilon
17	224448_s_at	MNF1	mitochondrial nucleoid factor 1
18	201692_at	SIGMAR1	sigma non-opioid intracellular receptor 1
19	214321_at	NOV	nephroblastoma overexpressed
20	212625_at	STX10	syntaxin 10
21	235384_at	NUDT19	nudix (nucleoside diphosphate linked moiety X)-type motif 19
22	224610_at	SNHG1 /// SNORD22	/ small nucleolar RNA host gene 1 (non-protein coding) /// small nucleolar RNA host gene 22 (non-protein coding)
23	224791_at	ASAP1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1
24	201521_s_at	NCBP2	nuclear cap binding protein subunit 2, 20kDa
25	214073_at	CTTN	cortactin
26	230424_at	NREP	neuronal regeneration related protein homolog (rat)
27	225540_at	MAP2	microtubule-associated protein 2
28	210811_s_at	DDX49	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49
29	212985_at	APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2
30	202208_s_at	ARL4C	ADP-ribosylation factor-like 4C
31	203578_s_at	SLC7A6	solute carrier family 7 (amino acid transporter light chain, y+L system)
32	218237_s_at	SLC38A1	solute carrier family 38, member 1
33	225676_s_at	DCAF13	DDB1 and CUL4 associated factor 13
34	203536_s_at	CIAO1	cytosolic iron-sulfur protein assembly 1
35	214039_s_at	LAPTM4B	lysosomal protein transmembrane 4 beta
36	236565_s_at	LARP6	La ribonucleoprotein domain family, member 6
37	226255_at	ZBTB33	zinc finger and BTB domain containing 33
38	207746_at	POLQ	polymerase (DNA directed), theta
39	201298_s_at	MOB1A	MOB kinase activator 1A
40	204649_at	TROAP	trophinin associated protein (tastin)
41	210416_s_at	CHEK2	checkpoint kinase 2
42	226847_at	FST	follistatin
43	224564_s_at	RTN3	reticulon 3
44	225424_at	GPAM	glycerol-3-phosphate acyltransferase, mitochondrial
45	230696_at	LOC100289092	uncharacterized LOC100289092
46	217861_s_at	PREB	prolactin regulatory element binding
47	244427_at	KIF23	Kinesin family member 23

1	212800_at	STX6	syntaxin 6
2	241453_at	LOC100653024	/// LOC uncharacterized LOC100653024 /// uncharacterized LOC1006531
3	217094_s_at	ITCH	itchy E3 ubiquitin protein ligase
4	227651_at	NACC1	nucleus accumbens associated 1, BEN and BTB (POZ) domain containing
5	203422_at	POLD1	polymerase (DNA directed), delta 1, catalytic subunit
6	224684_at	SNX12	sorting nexin 12
7	228238_at	GAS5	/// SNORD44 /// growth arrest-specific 5 (non-protein coding) /// small nucleolar RNA
8	229647_at	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-
9	220051_at	PRSS21	protease, serine, 21 (testisin)
10	212405_s_at	METTL13	methyltransferase like 13
11	225143_at	SFXN4	sideroflexin 4
12	218133_s_at	NIF3L1	NIF3 NGG1 interacting factor 3-like 1 (<i>S. cerevisiae</i>)
13	213310_at	EIF2C2	/// LOC286109 Eukaryotic translation initiation factor 2C, 2 /// Uncharacterized L
14	204480_s_at	C9orf16	chromosome 9 open reading frame 16
15	204608_at	ASL	argininosuccinate lyase
16	217926_at	C19orf53	chromosome 19 open reading frame 53
17	225081_s_at	CDCA7L	cell division cycle associated 7-like
18	201250_s_at	SLC2A1	solute carrier family 2 (facilitated glucose transporter), member 1
19	200827_at	PLOD1	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1
20	226938_at	DCAF4	DDB1 and CUL4 associated factor 4
21	202918_s_at	HSPE1-MOB4	/// MOB HSPE1-MOB4 readthrough /// MOB family member 4, phoein
22	225468_at	PATL1	protein associated with topoisomerase II homolog 1 (yeast)
23	202804_at	ABCC1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1
24	226355_at	POC1A	POC1 centriolar protein homolog A (<i>Chlamydomonas</i>)
25	222530_s_at	MKKS	McKusick-Kaufman syndrome
26	224598_at	MGAT4B	mannosyl (alpha-1,3)-glycoprotein beta-1,4-N-acetylglucosaminidase
27	217784_at	YKT6	YKT6 v-SNARE homolog (<i>S. cerevisiae</i>)
28	229671_s_at	MIS18A	MIS18 kinetochore protein homolog A (<i>S. pombe</i>)
29	219348_at	USE1	unconventional SNARE in the ER 1 homolog (<i>S. cerevisiae</i>)
30	217860_at	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kD
31	223389_s_at	ZNF581	zinc finger protein 581
32	225864_at	FAM84B	family with sequence similarity 84, member B
33	200868_s_at	RNF114	ring finger protein 114
34	231784_s_at	DCAF13	DDB1 and CUL4 associated factor 13
35	203588_s_at	TFDP2	transcription factor Dp-2 (E2F dimerization partner 2)
36	227103_s_at	ECE2	endothelin converting enzyme 2
37	218388_at	PGLS	6-phosphogluconolactonase
38	204407_at	TTF2	transcription termination factor, RNA polymerase II
39	201791_s_at	DHCR7	7-dehydrocholesterol reductase
40	232596_at	DIAPH3	diaphanous homolog 3 (<i>Drosophila</i>)
41	224615_x_at	HM13	histocompatibility (minor) 13
42	224890_s_at	C7orf59	chromosome 7 open reading frame 59
43	222451_s_at	ZDHHC9	zinc finger, DHHC-type containing 9
44	201066_at	CYC1	cytochrome c-1
45	202888_s_at	ANPEP	alanyl (membrane) aminopeptidase
46	200979_at	PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1
47	230032_at	OSGEPL1	O-sialoglycoprotein endopeptidase-like 1

1	211964_at	COL4A2	collagen, type IV, alpha 2
2	204717_s_at	SLC29A2	solute carrier family 29 (nucleoside transporters), member 2
3	212020_s_at	MKI67	antigen identified by monoclonal antibody Ki-67
4	218003_s_at	FKBP3 /// LOC10065286	FK506 binding protein 3, 25kDa /// uncharacterized LOC10065286
5	220189_s_at	MGAT4B	mannosyl (alpha-1,3)-glycoprotein beta-1,4-N-acetylglucosaminidase
6	201690_s_at	TPD52	tumor protein D52
7	219531_at	CEP72	centrosomal protein 72kDa
8	242828_at	FIGN	fidgetin
9	201710_at	MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2
10	211031_s_at	CLIP2	CAP-GLY domain containing linker protein 2
11	229268_at	FAM105B	family with sequence similarity 105, member B
12	235648_at	ZNF567	zinc finger protein 567
13	218343_s_at	GTF3C3	general transcription factor IIIC, polypeptide 3, 102kDa
14	212541_at	FLAD1	FAD1 flavin adenine dinucleotide synthetase homolog (S. cerevisiae)
15	226032_at	CASP2	caspase 2, apoptosis-related cysteine peptidase
16	201754_at	COX6C	cytochrome c oxidase subunit VIc
17	222155_s_at	SLC52A2	solute carrier family 52, riboflavin transporter, member 2
18	230249_at	KHDRBS3	KH domain containing, RNA binding, signal transduction associate
19	213127_s_at	MED8	mediator complex subunit 8
20	241908_at	BROX	BRO1 domain and CAAX motif containing
21	229665_at	CSTF3	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa
22	201479_at	DKC1 /// SNORA56	dyskeratosis congenita 1, dyskerin /// small nucleolar RNA, H/ACA
23	201275_at	FDPS	farnesyl diphosphate synthase
24	238273_at	C7orf73 /// LOC10028	chromosome 7 open reading frame 73 /// chromosome 7 open reading frame 73
25	243531_at	ORAOV1	oral cancer overexpressed 1
26	222987_s_at	TMEM9	transmembrane protein 9
27	209054_s_at	WHSC1	Wolf-Hirschhorn syndrome candidate 1
28	226649_at	PANK1	pantothenate kinase 1
29	205395_s_at	MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)
30	39729_at	PRDX2	peroxiredoxin 2
31	208934_s_at	LGALS8	lectin, galactoside-binding, soluble, 8
32	203167_at	TIMP2	TIMP metallopeptidase inhibitor 2
33	210290_at	ZNF174	zinc finger protein 174
34	224185_at	WRAP53	WD repeat containing, antisense to TP53
35	226630_at	MIS18BP1	MIS18 binding protein 1
36	228972_at	PITPNA-AS1	PITPNA antisense RNA 1 (non-protein coding)
37	210685_s_at	UBE4B	ubiquitination factor E4B
38	213754_s_at	PAIP1	poly(A) binding protein interacting protein 1
39	225196_s_at	MRPS26	mitochondrial ribosomal protein S26
40	202847_at	PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)
41	219004_s_at	MIS18A	MIS18 kinetochore protein homolog A (S. pombe)
42	227160_s_at	NDUFAF5	NADH dehydrogenase (ubiquinone) complex I, assembly factor 5
43	200734_s_at	ARF3	ADP-ribosylation factor 3
44	210418_s_at	IDH3B	isocitrate dehydrogenase 3 (NAD ⁺) beta
45	210470_x_at	NONO	non-POU domain containing, octamer-binding
46	65588_at	LOC388796	uncharacterized LOC388796
47	206273_at	SLMO1	slowmo homolog 1 (Drosophila)

1	222018_at	NACA	nascent polypeptide-associated complex alpha subunit
2	212072_s_at	CSNK2A1	/// CSNK2A1 casein kinase 2, alpha 1 polypeptide /// casein kinase 2, alpha 1 polypeptide (prosome, macropain) 26S subunit, ATPase, 2
3	201068_s_at	PSMC2	proteasome (prosome, macropain) 26S subunit, ATPase, 2
4	213419_at	APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2
5	32723_at	CSTF1	cleavage stimulation factor, 3' pre-RNA, subunit 1, 50kDa
6	211056_s_at	SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha steroid hydroxylase, irre like (Drosophila))
7	225303_at	KIRREL	chromodomain helicase DNA binding protein 7
8	218829_s_at	CHD7	BCL2-antagonist/killer 1
9	203728_at	BAK1	glutathione S-transferase mu 3 (brain)
10	202554_s_at	GSTM3	RNA binding motif protein 15
11	1555760_a_at	RBM15	KLHL23 /// PHOSPHO2 kelch-like 23 (Drosophila) /// PHOSPHO2-KLHL23 readthrough
12	213610_s_at	BOLA1	bola homolog 1 (E. coli)
13	233058_at	GPSM2	G-protein signaling modulator 2
14	232881_at	GNAS-AS1	GNAS antisense RNA 1 (non-protein coding)
15	224580_at	SLC38A1	solute carrier family 38, member 1
16	225925_s_at	USP48	ubiquitin specific peptidase 48
17	209171_at	ITPA	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)
18	218497_s_at	RNASEH1	ribonuclease H1
19	1553099_at	TIGD1	tigger transposable element derived 1
20	225777_at	SAPCD2	suppressor APC domain containing 2
21	227385_at	PPAPDC2	phosphatidic acid phosphatase type 2 domain containing 2
22	57703_at	SENP5	SUMO1/sentrin specific peptidase 5
23	217895_at	PTCD3	pentatricopeptide repeat domain 3
24	1558508_a_at	C1orf53	chromosome 1 open reading frame 53
25	214173_x_at	URI1	URI1, prefoldin-like chaperone
26	204514_at	DPH2	DPH2 homolog (S. cerevisiae)
27	219880_at	LOC100507619	uncharacterized LOC100507619
28	203550_s_at	FAM189B	family with sequence similarity 189, member B
29	202382_s_at	GNPDA1	glucosamine-6-phosphate deaminase 1
30	218538_s_at	MRS2	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)
31	220525_s_at	AUP1	ancient ubiquitous protein 1
32	220399_at	LINC00115	long intergenic non-protein coding RNA 115
33	219491_at	LRFN4	leucine rich repeat and fibronectin type III domain containing 4
34	222233_s_at	DCLRE1C	DNA cross-link repair 1C
35	214700_x_at	RIF1	RAP1 interacting factor homolog (yeast)
36	220160_s_at	KPTN	kaptin (actin binding protein)
37	223513_at	CENPJ	centromere protein J
38	1554408_a_at	TK1	thymidine kinase 1, soluble
39	212832_s_at	CKAP5	cytoskeleton associated protein 5
40	213571_s_at	EIF4E2	/// LOC100507406 eukaryotic translation initiation factor 4E family member 2 /// uncharacterized
41	212008_at	UBXN4	UBX domain protein 4
42	1554063_at	ZHX1-C8ORF76	ZHX1-C8ORF76 readthrough
43	204849_at	DPH3P1	/// TCFL5 DPH3, KTI11 homolog (S. cerevisiae) pseudogene 1 /// transcript
44	219002_at	FASTKD1	FAST kinase domains 1
45	219061_s_at	LAGE3	L antigen family, member 3
46	201509_at	IDH3B	isocitrate dehydrogenase 3 (NAD ⁺) beta

1	237005_at	LOC442075	uncharacterized LOC442075
2	225861_at	FAM195A	family with sequence similarity 195, member A
3	204871_at	MTERF	mitochondrial transcription termination factor
4	203390_s_at	KIF3C	kinesin family member 3C
5	223811_s_at	GET4 /// SUN1	golgi to ER traffic protein 4 homolog (S. cerevisiae) /// Sad1 and U
6	222654_at	IMPAD1	inositol monophosphatase domain containing 1
7	202528_at	GALE	UDP-galactose-4-epimerase
8	202645_s_at	MEN1	multiple endocrine neoplasia I
9	225692_at	CAMTA1	calmodulin binding transcription activator 1
10	1554026_a_at	MYO10	myosin X
11	227094_at	DHTKD1	dehydrogenase E1 and transketolase domain containing 1
12	209797_at	CNPY2	canopy 2 homolog (zebrafish)
13	228987_at	FAM49B	family with sequence similarity 49, member B
14	217950_at	NOSIP	nitric oxide synthase interacting protein
15	201558_at	RAE1	RAE1 RNA export 1 homolog (S. pombe)
16	230521_at	C9orf100	chromosome 9 open reading frame 100
17	217208_s_at	DLG1	discs, large homolog 1 (Drosophila)
18	218617_at	TRIT1	tRNA isopentenyltransferase 1
19	227724_at	LOC728190	uncharacterized LOC728190
20	212012_at	PXDN	peroxidasin homolog (Drosophila)
21	228543_at	PET117	PET117 homolog (S. cerevisiae)
22	209899_s_at	PUF60	poly-U binding splicing factor 60kDa
23	203706_s_at	FZD7	frizzled family receptor 7
24	226346_at	MEX3A	mex-3 homolog A (C. elegans)
25	208952_s_at	LARP4B	La ribonucleoprotein domain family, member 4B
26	227818_at	CEP85	centrosomal protein 85kDa
27	229981_at	SNX5	sorting nexin 5
28	211527_x_at	VEGFA	vascular endothelial growth factor A
29	229538_s_at	IQGAP3	IQ motif containing GTPase activating protein 3
30	202338_at	TK1	thymidine kinase 1, soluble
31	221908_at	RNFT2	ring finger protein, transmembrane 2
32	217043_s_at	MFN1	mitofusin 1
33	45714_at	HCFC1R1	host cell factor C1 regulator 1 (XPO1 dependent)
34	1553715_s_at	FAM195A	family with sequence similarity 195, member A
35	242592_at	GPR137C	G protein-coupled receptor 137C
36	228066_at	C17orf96	chromosome 17 open reading frame 96
37	213668_s_at	SOX4	SRY (sex determining region Y)-box 4
38	226086_at	SYT13	synaptotagmin XIII
39	224790_at	ASAP1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1
40	211165_x_at	EPHB2	EPH receptor B2
41	238768_at	C2orf68	chromosome 2 open reading frame 68
42	212757_s_at	CAMK2G	calcium/calmodulin-dependent protein kinase II gamma
43	218567_x_at	DPP3	dipeptidyl-peptidase 3
44	31807_at	DDX49	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49
45	1555274_a_at	EPT1	ethanolaminephosphotransferase 1 (CDP-ethanolamine-specific)
46	202261_at	VPS72	vacuolar protein sorting 72 homolog (S. cerevisiae)
47	207098_s_at	MFN1	mitofusin 1

1	214264_s_at	EFCAB11	EF-hand calcium binding domain 11
2	223530_at	TDRKH	tudor and KH domain containing
3	221649_s_at	PPAN /// PPAN-P2RY1	peter pan homolog (Drosophila) /// PPAN-P2RY11 readthrough
4	209588_at	EPHB2	EPH receptor B2
5	210014_x_at	IDH3B	isocitrate dehydrogenase 3 (NAD+) beta
6	202486_at	AFG3L2	AFG3 ATPase family gene 3-like 2 (S. cerevisiae)
7	229980_s_at	SNX5	sorting nexin 5
8	212858_at	PAQR4	progestin and adiponectin receptor family member IV
9	210785_s_at	C1orf38	chromosome 1 open reading frame 38
10	202758_s_at	RFXANK	regulatory factor X-associated ankyrin-containing protein
11	218522_s_at	MAP1S	microtubule-associated protein 1S
12	231967_at	PHF20L1	PHD finger protein 20-like 1
13	227456_s_at	C6orf136	chromosome 6 open reading frame 136
14	218016_s_at	POLR3E	polymerase (RNA) III (DNA directed) polypeptide E (80kD)
15	222759_at	SUV420H1	suppressor of variegation 4-20 homolog 1 (Drosophila)
16	200778_s_at	SEPT2	septin 2
17	232740_at	MCM3AP-AS1	MCM3AP antisense RNA 1 (non-protein coding)
18	217310_s_at	FOXJ3	forkhead box J3
19	219984_s_at	HRASLS	HRAS-like suppressor
20	203805_s_at	FANCA	Fanconi anemia, complementation group A
21	203438_at	STC2	stanniocalcin 2
22	202735_at	EBP	emopamil binding protein (sterol isomerase)
23	201341_at	ENC1	ectodermal-neural cortex 1 (with BTB-like domain)
24	225150_s_at	RTKN	rhotekin
25	213526_s_at	LIN37	lin-37 homolog (C. elegans)
26	201548_s_at	KDM5B	lysine (K)-specific demethylase 5B
27	221082_s_at	NDRG3	NDRG family member 3
28	228499_at	PFKFB4	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4
29	232652_x_at	SCAND1	SCAN domain containing 1
30	207571_x_at	C1orf38	chromosome 1 open reading frame 38
31	1555500_s_at	SLC2A4RG	SLC2A4 regulator
32	1554348_s_at	CDKN2AIPNL	CDKN2A interacting protein N-terminal like
33	213378_s_at	DDX11 /// DDX12P	DDX11 /// DDX12P /// DEAD/H (Asp-Glu-Ala-Asp/His) box helicase 11 /// DEAD/H (Asp-G
34	1555797_a_at	ARPC5	actin related protein 2/3 complex, subunit 5, 16kDa
35	219556_at	C16orf59	chromosome 16 open reading frame 59
36	203806_s_at	FANCA	Fanconi anemia, complementation group A
37	206949_s_at	RUSC1	RUN and SH3 domain containing 1
38	226569_s_at	CHTF18	CTF18, chromosome transmission fidelity factor 18 homolog (S. cerevisiae)
39	204078_at	LEPREL4	leprecan-like 4
40	1558329_at	TONSL	tonsoku-like, DNA repair protein
41	200709_at	FKBP1A	FK506 binding protein 1A, 12kDa
42	223528_s_at	METTL17	methyltransferase like 17
43	210463_x_at	TRMT1	tRNA methyltransferase 1 homolog (S. cerevisiae)
44	231146_at	FAM24B	family with sequence similarity 24, member B
45	204432_at	SOX12	SRY (sex determining region Y)-box 12
46	218206_x_at	SCAND1	SCAN domain containing 1
47	209705_at	MTF2	metal response element binding transcription factor 2

1	227348_at	PARS2	prolyl-tRNA synthetase 2, mitochondrial (putative)
2	226775_at	ENY2	enhancer of yellow 2 homolog (Drosophila)
3	1553015_a_at	RECQL4	RecQ protein-like 4
4	225362_at	FAM122B	family with sequence similarity 122B
5	228906_at	TET1	tet methylcytosine dioxygenase 1
6	1558143_a_at	BCL2L11	BCL2-like 11 (apoptosis facilitator)
7	238333_s_at	MTG1	Mitochondrial GTPase 1 homolog (S. cerevisiae)
8	34868_at	SMG5	smg-5 homolog, nonsense mediated mRNA decay factor (C. elegans)
9	200990_at	TRIM28	tripartite motif containing 28
10	219080_s_at	CTPS2	CTP synthase 2
11	223255_at	G2E3	G2/M-phase specific E3 ubiquitin protein ligase
12	210656_at	EED	embryonic ectoderm development
13	219615_s_at	KCNK5	potassium channel, subfamily K, member 5
14	221004_s_at	ITM2C	integral membrane protein 2C
15	209205_s_at	LMO4	LIM domain only 4
16	214185_at	KHDRBS1	KH domain containing, RNA binding, signal transduction associate
17	221906_at	TXNRD3 /// TXNRD3N1	thioredoxin reductase 3 /// thioredoxin reductase 3 neighbor
18	217714_x_at	STMN1	microRNA 3917 /// stathmin 1
19	207812_s_at	GORASP2	golgi reassembly stacking protein 2, 55kDa
20	203262_s_at	FAM50A	family with sequence similarity 50, member A
21	212809_at	NFATC2IP	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent
22	201948_at	GNL2	guanine nucleotide binding protein-like 2 (nucleolar)
23	44669_at	SDHAF1	succinate dehydrogenase complex assembly factor 1
24	200661_at	CTSA	cathepsin A
25	242560_at	FANCD2	Fanconi anemia, complementation group D2
26	202282_at	HSD17B10	hydroxysteroid (17-beta) dehydrogenase 10
27	212276_at	LPIN1	lipin 1
28	1553220_at	FAM117B	family with sequence similarity 117, member B
29	224652_at	CCNY	cyclin Y
30	41047_at	C9orf16	chromosome 9 open reading frame 16
31	222343_at	BCL2L11	BCL2-like 11 (apoptosis facilitator)
32	231895_at	SASS6	spindle assembly 6 homolog (C. elegans)
33	229099_at	C11orf83	chromosome 11 open reading frame 83
34	229672_at	UQCC	ubiquinol-cytochrome c reductase complex chaperone
35	61732_r_at	IFT74	intraflagellar transport 74 homolog (Chlamydomonas)
36	228259_s_at	EPB41L4A-AS1	EPB41L4A antisense RNA 1 (non-protein coding)
37	240228_at	CSMD3	CUB and Sushi multiple domains 3
38	204301_at	KBTBD11	kelch repeat and BTB (POZ) domain containing 11
39	210791_s_at	ARHGAP32	Rho GTPase activating protein 32
40	1563502_at	ZDHHC2	Zinc finger, DHHC-type containing 2
41	1569262_x_at	UBE3D	ubiquitin protein ligase E3D
42	206030_at	ASPA	aspartoacylase
43	1564372_s_at	CASC2	cancer susceptibility candidate 2 (non-protein coding)
44	1555352_at	FOXP2	forkhead box P2
45	205116_at	LAMA2	laminin, alpha 2
46	219332_at	MICALL2	MICAL-like 2
47	218483_s_at	IFT46	intraflagellar transport 46 homolog (Chlamydomonas)

1	225539_at	ZNF295	zinc finger protein 295
2	219415_at	TTYH1	tweety homolog 1 (Drosophila)
3	213519_s_at	LAMA2	laminin, alpha 2
4	203233_at	IL4R	interleukin 4 receptor
5	225999_at	RIMKLB	ribosomal modification protein rimK-like family member B
6	238484_s_at	SSBP2	single-stranded DNA binding protein 2
7	213228_at	PDE8B	phosphodiesterase 8B
8	1557132_at	WDR17	WD repeat domain 17
9	200704_at	LITAF	lipopolysaccharide-induced TNF factor
10	235335_at	ABCA9	ATP-binding cassette, sub-family A (ABC1), member 9
11	219954_s_at	GBA3	glucosidase, beta, acid 3 (cytosolic)
12	1554117_at	CCDC60	coiled-coil domain containing 60
13	205241_at	SCO2	SCO cytochrome oxidase deficient homolog 2 (yeast)
14	202972_s_at	FAM13A	family with sequence similarity 13, member A
15	205632_s_at	PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase, type I, beta
16	201042_at	TGM2	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glu
17	203151_at	MAP1A	microtubule-associated protein 1A
18	231434_at	LOC100505841	zinc finger protein 474-like
19	224648_at	GPBP1	GC-rich promoter binding protein 1
20	1561928_s_at	ANKUB1	ankyrin repeat and ubiquitin domain containing 1
21	238810_at	RFX3	regulatory factor X, 3 (influences HLA class II expression)
22	201924_at	AFF1	AF4/FMR2 family, member 1
23	1553798_a_at	FBXL13	F-box and leucine-rich repeat protein 13
24	242323_at	PLA2G12A	phospholipase A2, group XIIA
25	234605_at	CDC14B	CDC14 cell division cycle 14 homolog B (S. cerevisiae)
26	229956_at	NR2C1	nuclear receptor subfamily 2, group C, member 1
27	220500_s_at	RABL2A /// RABL2B	RAB, member of RAS oncogene family-like 2A /// RAB, member of
28	1552993_at	DYDC1	DPY30 domain containing 1
29	208866_at	CSNK1A1	casein kinase 1, alpha 1
30	1559067_a_at	LOC158402	Uncharacterized LOC158402
31	230351_at	LOC283481	uncharacterized LOC283481
32	1557285_at	AREGB	Amphiregulin B
33	238483_at	SSBP2	single-stranded DNA binding protein 2
34	202284_s_at	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
35	1562301_at	C8orf34	chromosome 8 open reading frame 34
36	208070_s_at	REV3L	REV3-like, polymerase (DNA directed), zeta, catalytic subunit
37	204497_at	ADCY9	adenylate cyclase 9
38	209612_s_at	ADH1B	alcohol dehydrogenase 1B (class I), beta polypeptide
39	1553228_at	CCDC89	coiled-coil domain containing 89
40	219970_at	GIPC2	GIPC PDZ domain containing family, member 2
41	204874_x_at	BAIAP3	BAI1-associated protein 3
42	202552_s_at	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)
43	231961_at	RBPMS	RNA binding protein with multiple splicing
44	210176_at	TLR1	toll-like receptor 1
45	235328_at	PLXNC1	Plexin C1
46	45288_at	ABHD6	abhydrolase domain containing 6
47	240303_at	TMC5	transmembrane channel-like 5

1	224165_s_at	IQCH	IQ motif containing H
2	215321_at	RUND3B	RUN domain containing 3B
3	218730_s_at	OGN	osteoglycin
4	202588_at	AK1	adenylate kinase 1
5	201983_s_at	EGFR	epidermal growth factor receptor
6	229064_s_at	RCAN3	RCAN family member 3
7	220050_at	C9orf9	chromosome 9 open reading frame 9
8	229573_at	USP9X	ubiquitin specific peptidase 9, X-linked
9	206914_at	CRTAM	cytotoxic and regulatory T cell molecule
10	225747_at	COQ10A	coenzyme Q10 homolog A (S. cerevisiae)
11	237298_at	FLJ26850	FLJ26850 protein
12	1559097_at	C14orf64	chromosome 14 open reading frame 64
13	1553211_at	ANKFN1	ankyrin-repeat and fibronectin type III domain containing 1
14	230824_at	MARCH10	membrane-associated ring finger (C3HC4) 10, E3 ubiquitin protein
15	1554708_s_at	SPATA6L	spermatogenesis associated 6-like
16	242009_at	SLC6A4	solute carrier family 6 (neurotransmitter transporter, serotonin), 4
17	35846_at	THRA	thyroid hormone receptor, alpha
18	242669_at	UFM1	Ubiquitin-fold modifier 1
19	226646_at	KLF2	Kruppel-like factor 2 (lung)
20	224175_s_at	TRIM34	TRIM34 /// TRIM6-TRI tripartite motif containing 34 /// TRIM6-TRIM34 readthrough
21	217047_s_at	FAM13A	family with sequence similarity 13, member A
22	202035_s_at	SFRP1	secreted frizzled-related protein 1
23	221766_s_at	FAM46A	family with sequence similarity 46, member A
24	204526_s_at	TBC1D8	TBC1 domain family, member 8 (with GRAM domain)
25	238854_at	LOC100506668	uncharacterized LOC100506668
26	205583_s_at	ALG13	asparagine-linked glycosylation 13 homolog (S. cerevisiae)
27	227415_at	LOC283508	uncharacterized LOC283508
28	1562640_at	HOXA-AS2	HOXA cluster antisense RNA 2 (non-protein coding)
29	228748_at	CD59	CD59 molecule, complement regulatory protein
30	226717_at	LRTOMT	leucine rich transmembrane and 0-methyltransferase domain con
31	212993_at	NACC2	NACC family member 2, BEN and BTB (POZ) domain containing
32	208707_at	EIF5	eukaryotic translation initiation factor 5
33	217437_s_at	TACC1	transforming, acidic coiled-coil containing protein 1
34	204713_s_at	F5	coagulation factor V (proaccelerin, labile factor)
35	202962_at	KIF13B	kinesin family member 13B
36	224588_at	XIST	X (inactive)-specific transcript (non-protein coding)
37	236016_at	SMARCE1	SWI/SNF related, matrix associated, actin dependent regulator of
38	224391_s_at	SIAE	sialic acid acetyltransferase
39	1557122_s_at	GABRB2	gamma-aminobutyric acid (GABA) A receptor, beta 2
40	231300_at	C16orf93	chromosome 16 open reading frame 93
41	213558_at	PCLO	piccolo (presynaptic cytomatrix protein)
42	219795_at	SLC6A14	solute carrier family 6 (amino acid transporter), member 14
43	202663_at	WIPF1	WAS/WASL interacting protein family, member 1
44	1563961_at	FHAD1	forkhead-associated (FHA) phosphopeptide binding domain 1
45	243413_at	TTC30B	tetratricopeptide repeat domain 30B
46	1560458_s_at	CAPS2	calcypbosine 2
47	231051_at	M1	uncharacterized LOC100507027

1	220218_at	SPATA6L	spermatogenesis associated 6-like
2	209977_at	PLG	plasminogen
3	202551_s_at	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)
4	220272_at	BNC2	basonuclin 2
5	228905_at	PCM1	pericentriolar material 1
6	215806_x_at	TARP /// TRGC2	TCR gamma alternate reading frame protein /// T cell receptor ga
7	230964_at	FREM2	FRAS1 related extracellular matrix protein 2
8	1556907_at	ZNF474	zinc finger protein 474
9	231136_at	MIR30C2	microRNA 30c-2
10	206010_at	HABP2	hyaluronan binding protein 2
11	1556325_at	FILIP1	filamin A interacting protein 1
12	241705_at	ABCA5	ATP-binding cassette, sub-family A (ABC1), member 5
13	214607_at	PAK3	p21 protein (Cdc42/Rac)-activated kinase 3
14	205337_at	DCT	dopachrome tautomerase (dopachrome delta-isomerase, tyrosine
15	1562321_at	PDK4	pyruvate dehydrogenase kinase, isozyme 4
16	202995_s_at	FBLN1	fibulin 1
17	233915_at	KIAA0825	KIAA0825
18	205198_s_at	ATP7A	ATPase, Cu++ transporting, alpha polypeptide
19	226228_at	AQP4	aquaporin 4
20	243423_at	TNIP1	TNFAIP3 interacting protein 1
21	231103_at	KCNN3	potassium intermediate/small conductance calcium-activated cha
22	227478_at	SETBP1	SET binding protein 1
23	212225_at	EIF1	eukaryotic translation initiation factor 1
24	206834_at	HBD	hemoglobin, delta
25	225102_at	MGLL	monoglyceride lipase
26	225250_at	STIM2	stromal interaction molecule 2
27	223905_at	CCDC135	coiled-coil domain containing 135
28	203787_at	SSBP2	single-stranded DNA binding protein 2
29	214438_at	HLX	H2.0-like homeobox
30	1565544_at	RNF141	ring finger protein 141
31	204674_at	LRMP	lymphoid-restricted membrane protein
32	225212_at	SLC25A25	solute carrier family 25 (mitochondrial carrier; phosphate carrier),
33	1556607_at	EHD4	EH-domain containing 4
34	227934_at	KPNA5	karyopherin alpha 5 (importin alpha 6)
35	205798_at	IL7R	interleukin 7 receptor
36	1558815_at	SORBS2	sorbin and SH3 domain containing 2
37	222892_s_at	TMEM40	transmembrane protein 40
38	233326_at	CCDC39	coiled-coil domain containing 39
39	235723_at	BNC2	basonuclin 2
40	205291_at	IL2RB	interleukin 2 receptor, beta
41	236745_at	CCDC78	coiled-coil domain containing 78
42	226956_at	MTMR3	myotubularin related protein 3
43	202393_s_at	KLF10	Kruppel-like factor 10
44	230891_at	TUBE1	Tubulin, epsilon 1
45	200911_s_at	TACC1	transforming, acidic coiled-coil containing protein 1
46	226992_at	NOSTRIN	nitric oxide synthase trafficker
47	226576_at	ARHGAP26	Rho GTPase activating protein 26

1	1553202_at	STOX1	storkhead box 1
2	223348_x_at	MUM1	melanoma associated antigen (mutated) 1
3	225624_at	SNX29	sorting nexin 29
4	219093_at	PID1	phosphotyrosine interaction domain containing 1
5	1553134_s_at	C9orf72	chromosome 9 open reading frame 72
6	214681_at	GK	glycerol kinase
7	230772_at	HNF4A	hepatocyte nuclear factor 4, alpha
8	228442_at	NFATC2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-depen
9	213527_s_at	ZNF688	zinc finger protein 688
10	202747_s_at	ITM2A	integral membrane protein 2A
11	203508_at	TNFRSF1B	tumor necrosis factor receptor superfamily, member 1B
12	201288_at	ARHGDI	Rho GDP dissociation inhibitor (GDI) beta
13	229994_at	NFIA	Nuclear factor I/A
14	236833_at	TTC16	tetratricopeptide repeat domain 16
15	230976_at	AK8	adenylate kinase 8
16	215046_at	KANSL1L	KAT8 regulatory NSL complex subunit 1-like
17	203845_at	KAT2B	K(lysine) acetyltransferase 2B
18	237420_at	ODF2L	outer dense fiber of sperm tails 2-like
19	229313_at	ANO5	anoctamin 5
20	228425_at	LOC654433	uncharacterized LOC654433
21	1558334_a_at	C22orf15	chromosome 22 open reading frame 15
22	202973_x_at	FAM13A	family with sequence similarity 13, member A
23	223322_at	RASSF5	Ras association (RalGDS/AF-6) domain family member 5
24	216109_at	MED13L	Mediator complex subunit 13-like
25	1552459_a_at	MBD3L1	methyl-CpG binding domain protein 3-like 1
26	225564_at	SPATA13	spermatogenesis associated 13
27	226430_at	RELL1	RELT-like 1
28	226991_at	NFATC2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-depen
29	235561_at	TXNL1	thioredoxin-like 1
30	213271_s_at	DOPEY1	dopey family member 1
31	224999_at	EGFR	epidermal growth factor receptor
32	227627_at	C8orf44-SGK3	/// SGK: C8orf44-SGK3 readthrough /// serum/glucocorticoid regulated kir
33	216840_s_at	LAMA2	laminin, alpha 2
34	219252_s_at	GEMIN8	gem (nuclear organelle) associated protein 8
35	213572_s_at	SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1
36	1563845_at	FAM153B	/// LOC1005 family with sequence similarity 153, member B /// uncharacterize
37	244289_at	ZNF300P1	zinc finger protein 300 pseudogene 1
38	243539_at	KIAA1841	KIAA1841
39	235465_at	FAM123A	family with sequence similarity 123A
40	240771_at	C1orf101	chromosome 1 open reading frame 101
41	221569_at	AHI1	Abelson helper integration site 1
42	221029_s_at	WNT5B	wingless-type MMTV integration site family, member 5B
43	231178_at	SPATA4	spermatogenesis associated 4
44	1552320_a_at	CCDC65	coiled-coil domain containing 65
45	228256_s_at	EPB41L4A	erythrocyte membrane protein band 4.1 like 4A
46	215232_at	ARHGAP44	Rho GTPase activating protein 44
47	209613_s_at	ADH1B	alcohol dehydrogenase 1B (class I), beta polypeptide

1	209960_at	HGF	hepatocyte growth factor (hepatopoietin A; scatter factor)
2	230511_at	CREM	cAMP responsive element modulator
3	213003_s_at	KIAA0146	KIAA0146
4	237282_s_at	AKAP14	A kinase (PRKA) anchor protein 14
5	213908_at	WHAMMP2 /// WHAN	WAS protein homolog associated with actin, golgi membranes and long intergenic non-protein coding RNA 472
6	220324_at	LINC00472	Bardet-Biedl syndrome 9
7	37547_at	BBS9	chromosome X open reading frame 22
8	1553905_at	CXorf22	serpin peptidase inhibitor, clade B (ovalbumin), member 1
9	212268_at	SERPINB1	G protein-coupled receptor 183
10	205419_at	GPR183	CD59 molecule, complement regulatory protein
11	212463_at	CD59	potassium voltage-gated channel, Shal-related subfamily, member 1
12	213832_at	KCND3	sex comb on midleg-like 4 (<i>Drosophila</i>)
13	1569225_a_at	SCML4	transducin (beta)-like 1X-linked
14	213400_s_at	TBL1X	family with sequence similarity 184, member A
15	220150_s_at	FAM184A	serpin peptidase inhibitor, clade B (ovalbumin), member 9
16	209723_at	SERPINB9	myelin protein zero-like 3
17	227747_at	MPZL3	ATPase, H ⁺ /K ⁺ exchanging, beta polypeptide
18	207546_at	ATP4B	chromosome 21 open reading frame 58
19	1555197_a_at	C21orf58	progesterone receptor
20	208305_at	PGR	PERP, TP53 apoptosis effector
21	236009_at	PERP	EF-hand domain (C-terminal) containing 1
22	225656_at	EFHC1	mohawk homeobox
23	239468_at	MKX	CUB and Sushi multiple domains 1
24	231223_at	CSMD1	WD repeat domain 66
25	1555007_s_at	WDR66	shisa homolog 6 (<i>Xenopus laevis</i>)
26	229266_at	SHISA6	lysophosphatidic acid receptor 1
27	204037_at	LPAR1	leucine rich repeat (in FLII) interacting protein 1
28	238840_at	LRRFIP1	galactose mutarotase (aldose 1-epimerase)
29	235256_s_at	GALM	hedgehog acyltransferase-like
30	223572_at	HHATL	sperm autoantigenic protein 17
31	205406_s_at	SPA17	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like
32	1554545_at	APOBEC4	BCL2-like 15
33	242013_at	BCL2L15	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6
34	209539_at	ARHGEF6	cripto, FRL-1, cryptic family 1 /// cripto, FRL-1, cryptic family 1B
35	223753_s_at	CFC1 /// CFC1B	uncharacterized LOC100133319
36	224110_at	PRO1804	adenosine deaminase, RNA-specific, B2
37	220648_at	ADARB2	PR domain containing 5
38	235764_at	PRDM5	Beta-2-microglobulin
39	232311_at	B2M	ankyrin 3, node of Ranvier (ankyrin G)
40	209442_x_at	ANK3	RNA binding protein with multiple splicing
41	209487_at	RBPM5	coiled-coil domain containing 67
42	1554072_s_at	CCDC67	zinc finger protein 273
43	215239_x_at	ZNF273	butyrophilin, subfamily 2, member A2
44	205298_s_at	BTN2A2	SAM domain, SH3 domain and nuclear localization signals 1
45	220330_s_at	SAMSN1	microtubule-associated protein 6
46	235672_at	MAP6	dopachrome tautomerase (dopachrome delta-isomerase, tyrosine
47	205338_s_at	DCT	

1	222520_s_at	IFT57	intraflagellar transport 57 homolog (Chlamydomonas)
2	244485_at	HLA-DPB1	major histocompatibility complex, class II, DP beta 1
3	213684_s_at	PDLIM5	PDZ and LIM domain 5
4	230839_at	PRMT8	protein arginine methyltransferase 8
5	201525_at	APOD	apolipoprotein D
6	230744_at	FSTL1	follistatin-like 1
7	204202_at	IQCE	IQ motif containing E
8	223706_at	C22orf23	chromosome 22 open reading frame 23
9	235048_at	FAM169A	family with sequence similarity 169, member A
10	229941_at	FAM166B	family with sequence similarity 166, member B
11	1556630_at	CASC2	cancer susceptibility candidate 2 (non-protein coding)
12	202902_s_at	CTSS	cathepsin S
13	1565149_at	DYNC2H1	dynein, cytoplasmic 2, heavy chain 1
14	211696_x_at	HBB	hemoglobin, beta
15	209655_s_at	TMEM47	transmembrane protein 47
16	202727_s_at	IFNGR1	interferon gamma receptor 1
17	206465_at	ACSBG1	acyl-CoA synthetase bubblegum family member 1
18	203969_at	PEX3	peroxisomal biogenesis factor 3
19	215342_s_at	RABGAP1L	RAB GTPase activating protein 1-like
20	206932_at	CH25H	cholesterol 25-hydroxylase
21	223059_s_at	FAM107B	family with sequence similarity 107, member B
22	232262_at	PIGL	phosphatidylinositol glycan anchor biosynthesis, class L
23	1556579_s_at	IGSF10	immunoglobulin superfamily, member 10
24	236098_at	C17orf110	chromosome 17 open reading frame 110
25	206194_at	HOXC4	homeobox C4
26	227337_at	ANKRD37	ankyrin repeat domain 37
27	1553423_a_at	SLFN13	schlafen family member 13
28	202157_s_at	CELF2	CUGBP, Elav-like family member 2
29	229430_at	C8orf46	chromosome 8 open reading frame 46
30	206335_at	GALNS	galactosamine (N-acetyl)-6-sulfate sulfatase
31	212486_s_at	FYN	FYN oncogene related to SRC, FGR, YES
32	210390_s_at	CCL14 /// CCL14-CCL1!	chemokine (C-C motif) ligand 14 /// CCL14-CCL15 readthrough ///
33	209978_s_at	LPA /// PLG	lipoprotein, Lp(a) /// plasminogen
34	201694_s_at	EGR1	early growth response 1
35	1556950_s_at	SERPINB6	serpin peptidase inhibitor, clade B (ovalbumin), member 6
36	230552_at	LOC100134317 /// LOC100134317	uncharacterized LOC100134317 /// uncharacterized LOC284412
37	211776_s_at	EPB41L3	erythrocyte membrane protein band 4.1-like 3
38	1559496_at	PPA2	pyrophosphatase (inorganic) 2
39	236029_at	FAT3	FAT tumor suppressor homolog 3 (Drosophila)
40	232109_at	UBXN10	UBX domain protein 10
41	203074_at	ANXA8 /// ANXA8L1	/ annexin A8 /// annexin A8-like 1 /// annexin A8-like 2
42	226653_at	MARK1	MAP/microtubule affinity-regulating kinase 1
43	236031_x_at	FREM1	FRAS1 related extracellular matrix 1
44	1552705_at	DUSP19	dual specificity phosphatase 19
45	223047_at	CMTM6	CKLF-like MARVEL transmembrane domain containing 6
46	241843_at	EIF5 /// SNORA28	eukaryotic translation initiation factor 5 /// small nucleolar RNA, f
47	219864_s_at	RCAN3	RCAN family member 3

1			
2	212779_at	KIAA1109	KIAA1109
3	219736_at	TRIM36	tripartite motif containing 36
4	231930_at	ELMOD1	ELMOD1 // LOC64392:ELMO/CED-12 domain containing 1 // uncharacterized LOC64392
5	210345_s_at	DNAH9	dynein, axonemal, heavy chain 9
6	204179_at	MB	myoglobin
7	1562336_at	CASC2	cancer susceptibility candidate 2 (non-protein coding)
8	205651_x_at	RAPGEF4	Rap guanine nucleotide exchange factor (GEF) 4
9	231909_x_at	ODF2L	outer dense fiber of sperm tails 2-like
10	230722_at	BNC2	basonuclin 2
11	215092_s_at	NFAT5	nuclear factor of activated T-cells 5, tonicity-responsive
12	223786_at	CHST6	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6
13	209823_x_at	HLA-DQB1	HLA-DQB1 // LOC100 major histocompatibility complex, class II, DQ beta 1 // HLA class
14	239151_at	LOC399753	uncharacterized LOC399753
15	1564474_at	ZBED3-AS1	ZBED3 antisense RNA 1 (non-protein coding)
16	205251_at	PER2	period homolog 2 (Drosophila)
17	220539_at	TTC40	tetratricopeptide repeat domain 40
18	218694_at	ARMCX1	armadillo repeat containing, X-linked 1
19	242482_at	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue
20	225283_at	ARRDC4	arrestin domain containing 4
21	201496_x_at	MYH11	myosin, heavy chain 11, smooth muscle
22	238158_at	MEIG1	meiosis expressed gene 1 homolog (mouse)
23	243649_at	FBXO7	F-box protein 7
24	218764_at	PRKCH	protein kinase C, eta
25	221207_s_at	NBEA	neurobeachin
26	241808_at	ZC2HC1A	zinc finger, C2HC-type containing 1A
27	201739_at	SGK1	serum/glucocorticoid regulated kinase 1
28	242344_at	GABRB2	gamma-aminobutyric acid (GABA) A receptor, beta 2
29	201721_s_at	LAPTM5	lysosomal protein transmembrane 5
30	1555112_a_at	C1orf114	chromosome 1 open reading frame 114
31	202018_s_at	LTF	lactotransferrin
32	216663_s_at	ZMYND10	zinc finger, MYND-type containing 10
33	205597_at	SLC44A4	solute carrier family 44, member 4
34	220908_at	CCDC33	coiled-coil domain containing 33
35	210538_s_at	BIRC3	baculoviral IAP repeat containing 3
36	205831_at	CD2	CD2 molecule
37	237755_s_at	WDR16	WD repeat domain 16
38	231875_at	KIF21A	kinesin family member 21A
39	241950_at	WWC1	WW and C2 domain containing 1
40	232731_x_at	LOC100190938	uncharacterized LOC100190938
41	212651_at	RHOBTB1	Rho-related BTB domain containing 1
42	234072_at	SEMA4A	sema domain, immunoglobulin domain (Ig), transmembrane dom
43	227830_at	GABRB3	gamma-aminobutyric acid (GABA) A receptor, beta 3
44	232461_at	AHI1	Abelson helper integration site 1
45	228577_x_at	ODF2L	outer dense fiber of sperm tails 2-like
46	220105_at	RTDR1	rhabdoid tumor deletion region gene 1
47	213910_at	IGFBP7	insulin-like growth factor binding protein 7
48	206693_at	IL7	interleukin 7

1	1556493_a_at	KDM4C	lysine (K)-specific demethylase 4C
2	236083_at	BCL2L15	BCL2-like 15
3	1559322_at	LOC727916	uncharacterized LOC727916
4	36711_at	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (av
5	241745_at	LOC100507557	uncharacterized LOC100507557
6	225939_at	EIF4E3	eukaryotic translation initiation factor 4E family member 3
7	219222_at	RBKS	ribokinase
8	207624_s_at	RPGR	retinitis pigmentosa GTPase regulator
9	237690_at	GPR115	G protein-coupled receptor 115
10	241731_x_at	ZNF440	zinc finger protein 440
11	1552448_a_at	C8orf12	chromosome 8 open reading frame 12
12	227098_at	DUSP18	dual specificity phosphatase 18
13	201693_s_at	EGR1	early growth response 1
14	204249_s_at	LMO2	LIM domain only 2 (rhombotin-like 1)
15	221180_at	YSK4	YSK4 Sps1/Ste20-related kinase homolog (S. cerevisiae)
16	1552950_at	C15orf26	chromosome 15 open reading frame 26
17	243582_at	SH3RF2	SH3 domain containing ring finger 2
18	223608_at	EFCAB2	EF-hand calcium binding domain 2
19	220003_at	LRRC36	leucine rich repeat containing 36
20	228476_at	KIAA1407	KIAA1407
21	210650_s_at	PCLO	piccolo (presynaptic cytomatrix protein)
22	213888_s_at	TRAF3IP3	TRAF3 interacting protein 3
23	228448_at	MAP6	microtubule-associated protein 6
24	212441_at	KIAA0232	KIAA0232
25	209970_x_at	CASP1	caspase 1, apoptosis-related cysteine peptidase
26	1556378_a_at	LOC440896	uncharacterized LOC440896
27	216979_at	NR4A3	nuclear receptor subfamily 4, group A, member 3
28	231026_at	EFHC1	EF-hand domain (C-terminal) containing 1
29	35974_at	LRMP	lymphoid-restricted membrane protein
30	205308_at	ZC2HC1A	zinc finger, C2HC-type containing 1A
31	212291_at	HIPK1	homeodomain interacting protein kinase 1
32	230561_s_at	KANSL1L	KAT8 regulatory NSL complex subunit 1-like
33	207789_s_at	DPP6	dipeptidyl-peptidase 6
34	1557207_s_at	LOC283177	uncharacterized LOC283177
35	222486_s_at	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1
36	238778_at	MPP7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily mem
37	1552384_a_at	FAM71A	family with sequence similarity 71, member A
38	220769_s_at	WDR78	WD repeat domain 78
39	1559756_at	DKFZp667F0711	uncharacterized protein DKFZp667F0711
40	228642_at	HOTAIRM1	HOXA transcript antisense RNA, myeloid-specific 1 (non-protein co
41	217671_at	DSERG1	Down syndrome encephalopathy related protein 1
42	205650_s_at	FGA	fibrinogen alpha chain
43	205366_s_at	HOXB6	homeobox B6
44	216356_x_at	BAIAP3	BAI1-associated protein 3
45	217995_at	SQRDL	sulfide quinone reductase-like (yeast)
46	232639_at	C3orf25	chromosome 3 open reading frame 25
47	221185_s_at	IQCG	IQ motif containing G

1	219777_at	GIMAP6	GTPase, IMAP family member 6
2	210839_s_at	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2
3	206363_at	MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)
4	1554980_a_at	ATF3	activating transcription factor 3
5	218584_at	TCTN1	tectonic family member 1
6	204057_at	IRF8	interferon regulatory factor 8
7	1557570_a_at	LOC285084	uncharacterized LOC285084
8	219563_at	LINC00341	long intergenic non-protein coding RNA 341
9	219584_at	PLA1A	phospholipase A1 member A
10	207797_s_at	LRP2BP	LRP2 binding protein
11	204703_at	IFT88	intraflagellar transport 88 homolog (Chlamydomonas)
12	1555564_a_at	CFI	complement factor I
13	220088_at	C5AR1	complement component 5a receptor 1
14	220271_x_at	EFCAB6	EF-hand calcium binding domain 6
15	219597_s_at	DUOX1	dual oxidase 1
16	223611_s_at	LNX1	ligand of numb-protein X 1, E3 ubiquitin protein ligase
17	238326_at	ODF3B	outer dense fiber of sperm tails 3B
18	204731_at	TGFBR3	transforming growth factor, beta receptor III
19	221290_s_at	MUM1	melanoma associated antigen (mutated) 1
20	230763_at	SPATA17	spermatogenesis associated 17
21	206974_at	CXCR6	chemokine (C-X-C motif) receptor 6
22	223731_at	MYCBPAP	MYCBP associated protein
23	226066_at	MITF	microphthalmia-associated transcription factor
24	213006_at	CEBDP	CCAAT/enhancer binding protein (C/EBP), delta
25	242268_at	CELF2	CUGBP, Elav-like family member 2
26	209616_s_at	CES1 /// LOC10065305	carboxylesterase 1 /// liver carboxylesterase 1-like
27	1564238_a_at	WDR49	WD repeat domain 49
28	226553_at	TMPRSS2	transmembrane protease, serine 2
29	205302_at	IGFBP1	insulin-like growth factor binding protein 1
30	230261_at	ST8SIA4	ST8 alpha-N-acetyl-neuraminate alpha-2,8-sialyltransferase 4
31	1553630_at	C10orf107	chromosome 10 open reading frame 107
32	236674_at	LOC388780	uncharacterized LOC388780
33	223940_x_at	LOC100507645 /// MA	uncharacterized LOC100507645 /// metastasis associated lung ad
34	217752_s_at	CNDP2	CNDP dipeptidase 2 (metallopeptidase M20 family)
35	212331_at	RBL2	retinoblastoma-like 2 (p130)
36	1559584_a_at	C16orf54	chromosome 16 open reading frame 54
37	223882_at	FAM172A	family with sequence similarity 172, member A
38	241495_at	CCNL1	cyclin L1
39	224021_at	RP1	retinitis pigmentosa 1 (autosomal dominant)
40	242979_at	IRS1	insulin receptor substrate 1
41	213784_at	IFT27	intraflagellar transport 27 homolog (Chlamydomonas)
42	225557_at	CSRNP1	cysteine-serine-rich nuclear protein 1
43	214734_at	EXPH5	exophilin 5
44	240033_at	PLG	plasminogen
45	236965_at	UBQLNL	ubiquilin-like
46	213186_at	DZIP3	DAZ interacting protein 3, zinc finger
47	231029_at	F5	coagulation factor V (proaccelerin, labile factor)

1	233057_at	HSPB8	heat shock 22kDa protein 8
2	221491_x_at	HLA-DRB1	/// HLA-DR1 major histocompatibility complex, class II, DR beta 1
3			/// major histocompatibility complex, class II, DR beta 1
4	231081_at	C2orf73	chromosome 2 open reading frame 73
5	230903_s_at	C8orf42	chromosome 8 open reading frame 42
6	214211_at	FTH1	ferritin, heavy polypeptide 1
7	228850_s_at	SLIT2	slit homolog 2 (<i>Drosophila</i>)
8	228316_at	C2orf63	chromosome 2 open reading frame 63
9	205011_at	VWA5A	von Willebrand factor A domain containing 5A
10	238909_at	S100A10	S100 calcium binding protein A10
11	242661_x_at	ALS2CR12	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, canary
12	213998_s_at	DDX17	DEAD (Asp-Glu-Ala-Asp) box helicase 17
13	235352_at	MR1	major histocompatibility complex, class I-related
14	227250_at	KREMEN1	kringle containing transmembrane protein 1
15	228496_s_at	CRIM1	Cysteine rich transmembrane BMP regulator 1 (chordin-like)
16	1557432_at	RASAL2	RAS protein activator like 2
17	205568_at	AQP9	aquaporin 9
18	1566079_at	RPS16P5	ribosomal protein S16 pseudogene 5
19	236166_at	LOC285147	uncharacterized LOC285147
20	214043_at	PTPRD	protein tyrosine phosphatase, receptor type, D
21	215133_s_at	FAM153A	/// FAM153 family with sequence similarity 153, member A
22			/// family with sequence similarity 153, member A
23	229953_x_at	LCA5	Leber congenital amaurosis 5
24	211795_s_at	FYB	FYN binding protein
25	213142_x_at	PION	pigeon homolog (<i>Drosophila</i>)
26	209821_at	IL33	interleukin 33
27	229378_at	STOX1	storkhead box 1
28	227265_at	FGL2	fibrinogen-like 2
29	238900_at	HLA-DRB1	/// HLA-DR1 major histocompatibility complex, class II, DR beta 1
30			/// major histocompatibility complex, class II, DR beta 1
31	209194_at	CETN2	centrin, EF-hand protein, 2
32	204749_at	NAP1L3	nucleosome assembly protein 1-like 3
33	227210_at	SFMBT2	Scm-like with four mbt domains 2
34	237328_at	C14orf105	chromosome 14 open reading frame 105
35	214748_at	N4BP2L2	NEDD4 binding protein 2-like 2
36	239458_at	ALS2CR12	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, canary
37	204783_at	MLF1	myeloid leukemia factor 1
38	228461_at	SH3RF3	SH3 domain containing ring finger 3
39	1553674_at	LRRIQ3	leucine-rich repeats and IQ motif containing 3
40	1557261_at	WHAMMP2	/// WHAM WAS protein homolog associated with actin, golgi membranes and
41			TNF receptor-associated factor 3 interacting protein 1
42	238494_at	TRAF3IP1	potassium channel tetramerisation domain containing 12
43	212192_at	KCTD12	chromosome 11 open reading frame 63
44	220141_at	C11orf63	major facilitator superfamily domain containing 4
45	229254_at	MFSD4	dystrophin
46	203881_s_at	DMD	family with sequence similarity 169, member A
47	213954_at	FAM169A	insulin receptor substrate 1
48	204686_at	IRS1	fibronectin type III and SPRY domain containing 1-like
49	242586_at	FSD1L	myosin light chain kinase 3
50	217623_at	MYLK3	transmembrane protein 45B
51	226226_at		
52			
53			
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1	230496_at	FAM123A	family with sequence similarity 123A
2	201843_s_at	EFEMP1	EGF containing fibulin-like extracellular matrix protein 1
3	242086_at	SPATA6	spermatogenesis associated 6
4	237285_at	SORBS2	sorbin and SH3 domain containing 2
5	219182_at	TMEM231	transmembrane protein 231
6	1563475_s_at	METTL20	methyltransferase like 20
7	236981_at	C17orf99	chromosome 17 open reading frame 99
8	219197_s_at	SCUBE2	signal peptide, CUB domain, EGF-like 2
9	1553765_a_at	KLHL32	kelch-like 32 (Drosophila)
10	235298_at	WDR27	WD repeat domain 27
11	1564093_at	NEK1	NIMA (never in mitosis gene a)-related kinase 1
12	204759_at	RCBTB2	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing 2
13	1556608_a_at	EHD4	EHD-domain containing 4
14	219578_s_at	CPEB1	cytoplasmic polyadenylation element binding protein 1
15	238447_at	RBMS3	RNA binding motif, single stranded interacting protein 3
16	1560119_at	LOC389634	uncharacterized LOC389634
17	236175_at	TRIM55	tripartite motif containing 55
18	214633_at	SOX3	SRY (sex determining region Y)-box 3
19	209897_s_at	SLIT2	slit homolog 2 (Drosophila)
20	244710_at	LRGUK	leucine-rich repeats and guanylate kinase domain containing 1
21	220244_at	LINC00312	long intergenic non-protein coding RNA 312
22	207961_x_at	MYH11	myosin, heavy chain 11, smooth muscle
23	232366_at	KIAA0232	KIAA0232
24	239870_at	SPATS1 /// TMEM151	spermatogenesis associated, serine-rich 1 /// transmembrane protein 151
25	236325_at	KIAA1377	KIAA1377
26	206076_at	LRRC23	leucine rich repeat containing 23
27	203518_at	LYST	lysosomal trafficking regulator
28	210800_at	TIMM8A	translocase of inner mitochondrial membrane 8 homolog A (yeast)
29	208078_s_at	SIK1	salt-inducible kinase 1
30	1561200_at	VWA3B	von Willebrand factor A domain containing 3B
31	201328_at	ETS2	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)
32	220252_x_at	CXorf21	chromosome X open reading frame 21
33	201301_s_at	ANXA4	annexin A4
34	1556477_a_at	LOC283485	uncharacterized LOC283485
35	231549_at	C1orf158	chromosome 1 open reading frame 158
36	205529_s_at	RUNX1T1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)
37	225502_at	DOCK8	dedicator of cytokinesis 8
38	242345_at	COL28A1	collagen, type XXVIII, alpha 1
39	201466_s_at	JUN	jun proto-oncogene
40	210222_s_at	RTN1	reticulon 1
41	220072_at	CSPP1	centrosome and spindle pole associated protein 1
42	1568924_a_at	IQUB	IQ motif and ubiquitin domain containing
43	211143_x_at	NR4A1	nuclear receptor subfamily 4, group A, member 1
44	241368_at	PLIN5	perilipin 5
45	203758_at	CTSO	cathepsin O
46	203474_at	IQGAP2	IQ motif containing GTPase activating protein 2
47	202587_s_at	AK1	adenylate kinase 1

1	207231_at	DZIP3	DAZ interacting protein 3, zinc finger
2	240282_at	WDR1	WD repeat domain 1
3	205948_at	PTPRT	protein tyrosine phosphatase, receptor type, T
4	222253_s_at	POM121L9P	POM121 transmembrane nucleoporin-like 9, pseudogene
5	227081_at	DNALI1	dynein, axonemal, light intermediate chain 1
6	243896_at	WDR96	WD repeat domain 96
7	233971_at	FAM166A	family with sequence similarity 166, member A
8	243758_at	CCDC37	coiled-coil domain containing 37
9	206938_at	SRD5A2	steroid-5-alpha-reductase, alpha polypeptide 2 (3-oxo-5 alpha-ste
10	226856_at	MUSTN1 /// TMEM11	musculoskeletal, embryonic nuclear protein 1 /// TMEM110-MUS
11	237585_at	C4orf47	chromosome 4 open reading frame 47
12	242907_at	GBP2	guanylate binding protein 2, interferon-inducible
13	225344_at	NCOA7	nuclear receptor coactivator 7
14	214192_at	NUP88	nucleoporin 88kDa
15	205476_at	CCL20	chemokine (C-C motif) ligand 20
16	222150_s_at	PION	pigeon homolog (Drosophila)
17	228600_x_at	FAM221A	family with sequence similarity 221, member A
18	201473_at	JUNB	jun B proto-oncogene
19	227690_at	GABRB3	gamma-aminobutyric acid (GABA) A receptor, beta 3
20	213922_at	TTBK2	tau tubulin kinase 2
21	206526_at	RIBC2	RIB43A domain with coiled-coils 2
22	213934_s_at	ZNF23	zinc finger protein 23 (KOX 16)
23	228056_s_at	NAPSB	napsin B aspartic peptidase pseudogene
24	240898_at	SPAG16	sperm associated antigen 16
25	57540_at	RBKS	ribokinase
26	206115_at	EGR3	early growth response 3
27	203543_s_at	KLF9	Kruppel-like factor 9
28	219049_at	CSGALNACT1	chondroitin sulfate N-acetylgalactosaminyltransferase 1
29	214811_at	RIMBP2	RIMS binding protein 2
30	242036_x_at	ATP2B3	ATPase, Ca++ transporting, plasma membrane 3
31	200904_at	HLA-E	major histocompatibility complex, class I, E
32	230142_s_at	CIRBP	cold inducible RNA binding protein
33	236519_at	C9orf135	chromosome 9 open reading frame 135
34	207075_at	NLRP3	NLR family, pyrin domain containing 3
35	238127_at	GAS6-AS1	GAS6 antisense RNA 1 (non-protein coding)
36	232777_s_at	C6orf118	chromosome 6 open reading frame 118
37	238430_x_at	SLFN5	schlafin family member 5
38	231043_at	PCDP1	primary ciliary dyskinesia protein 1
39	239043_at	ZNF404	zinc finger protein 404
40	205528_s_at	RUNX1T1	runt-related transcription factor 1; translocated to, 1 (cyclin D-rel;
41	206811_at	ADCY8	adenylate cyclase 8 (brain)
42	210032_s_at	SPAG6	sperm associated antigen 6
43	40284_at	FOXA2	forkhead box A2
44	218687_s_at	MUC13	mucin 13, cell surface associated
45	209116_x_at	HBB	hemoglobin, beta
46	221524_s_at	RRAGD	Ras-related GTP binding D
47	1559333_at	SRGAP3-AS2	SRGAP3 antisense RNA 2 (non-protein coding)

1	211200_s_at	EFCAB2	EF-hand calcium binding domain 2
2	239785_at	DZIP1L	DAZ interacting protein 1-like
3	1553684_at	PPIL6	peptidylprolyl isomerase (cyclophilin)-like 6
4	225328_at	FBXO32	F-box protein 32
5	209619_at	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain
6	205068_s_at	ARHGAP26	Rho GTPase activating protein 26
7	220344_at	C11orf16	chromosome 11 open reading frame 16
8	204863_s_at	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)
9	209921_at	SLC7A11	solute carrier family 7 (anionic amino acid transporter light chain, member 11)
10	229369_at	VSIG2	V-set and immunoglobulin domain containing 2
11	236421_at	ANKRD45	ankyrin repeat domain 45
12	231073_at	C1orf168	chromosome 1 open reading frame 168
13	222904_s_at	TMC5	transmembrane channel-like 5
14	220293_at	CATSPERB	CATSPER channel auxiliary subunit beta
15	1561096_at	LOC285419	uncharacterized LOC285419
16	224400_s_at	CHST9	carbohydrate (N-acetylgalactosamine 4-O) sulfotransferase 9
17	204002_s_at	ICA1	islet cell autoantigen 1, 69kDa
18	205860_x_at	FOLH1 /// FOLH1B	folate hydrolase (prostate-specific membrane antigen) 1 /// folate hydrolase (prostate-specific membrane antigen) 1B
19	1555246_a_at	SCN1A	sodium channel, voltage-gated, type I, alpha subunit
20	222314_x_at	EGOT	eosinophil granule ontology transcript (non-protein coding)
21	220581_at	CCDC170	coiled-coil domain containing 170
22	242807_at	FSD1L	fibronectin type III and SPRY domain containing 1-like
23	207072_at	IL18RAP	interleukin 18 receptor accessory protein
24	1556666_a_at	LOC100652860 /// LOC100652860	tetratricopeptide repeat protein 6-like /// tetratricopeptide repeat protein 6-like
25	209966_x_at	ESRRG	estrogen-related receptor gamma
26	228969_at	AGR2	anterior gradient 2 homolog (Xenopus laevis)
27	222220_s_at	TSNAXIP1	translin-associated factor X interacting protein 1
28	240830_at	SCARNA17	small Cajal body-specific RNA 17
29	1552325_at	CCDC11	coiled-coil domain containing 11
30	211471_s_at	RAB36	RAB36, member RAS oncogene family
31	221886_at	DENND2A	DENN/MADD domain containing 2A
32	205488_at	GZMA	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine protease)
33	225516_at	SLC7A2	solute carrier family 7 (cationic amino acid transporter, y ⁺ system)
34	243352_at	ALPK1	alpha-kinase 1
35	238581_at	GBP5	guanylate binding protein 5
36	203675_at	NUCB2	nucleobindin 2
37	202341_s_at	TRIM2	tripartite motif containing 2
38	205518_s_at	CMAHP	cytidine monophospho-N-acetylneuraminate hydroxylase, pseudogene
39	1560396_at	KLHL6	kelch-like 6 (Drosophila)
40	230180_at	DDX17	DEAD (Asp-Glu-Ala-Asp) box helicase 17
41	205016_at	TGFA	transforming growth factor, alpha
42	219583_s_at	SPATA7	spermatogenesis associated 7
43	232027_at	SYNE1	spectrin repeat containing, nuclear envelope 1
44	211105_s_at	NFATC1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1
45	213217_at	ADCY2	adenylate cyclase 2 (brain)
46	225061_at	DNAJA4	DnaJ (Hsp40) homolog, subfamily A, member 4
47	200811_at	CIRBP	cold inducible RNA binding protein

1	211654_x_at	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1
2	205101_at	CIITA	class II, major histocompatibility complex, transactivator
3	226187_at	CDS1	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) :
4	1557718_at	PPP2R5C	protein phosphatase 2, regulatory subunit B', gamma
5	1560426_at	C12orf55 /// C12orf63	chromosome 12 open reading frame 55 /// chromosome 12 open
6	205821_at	KLRC4-KLRK1	/// KLRK KLRC4-KLRK1 readthrough /// killer cell lectin-like receptor subfan
7	230931_at	PLG	plasminogen
8	220084_at	C14orf105	chromosome 14 open reading frame 105
9	229724_at	GABRB3	gamma-aminobutyric acid (GABA) A receptor, beta 3
10	210943_s_at	LYST	lysosomal trafficking regulator
11	227865_at	IDNK	idnK, gluconokinase homolog (E. coli)
12	227438_at	ALPK1	alpha-kinase 1
13	227727_at	MRGPRF	MAS-related GPR, member F
14	204363_at	F3	coagulation factor III (thromboplastin, tissue factor)
15	202036_s_at	SFRP1	secreted frizzled-related protein 1
16	215692_s_at	MPPED2	metallophosphoesterase domain containing 2
17	207584_at	LPA	lipoprotein, Lp(a)
18	206552_s_at	TAC1	tachykinin, precursor 1
19	229723_at	TAGAP	T-cell activation RhoGTPase activating protein
20	1553159_at	DNAH11	dynein, axonemal, heavy chain 11
21	205399_at	DCLK1	doublecortin-like kinase 1
22	216920_s_at	TARP /// TRGC2	TCR gamma alternate reading frame protein /// T cell receptor gamma
23	202191_s_at	GAS7	growth arrest-specific 7
24	1570289_at	LOC646736	uncharacterized LOC646736
25	203896_s_at	PLCB4	phospholipase C, beta 4
26	206169_x_at	ZC3H7B	zinc finger CCCH-type containing 7B
27	1555993_at	CACNA1D	calcium channel, voltage-dependent, L type, alpha 1D subunit
28	204813_at	MAPK10	mitogen-activated protein kinase 10
29	221523_s_at	RRAGD	Ras-related GTP binding D
30	1552825_at	ZNF396	zinc finger protein 396
31	222336_at	C4orf34	chromosome 4 open reading frame 34
32	235350_at	C4orf19	chromosome 4 open reading frame 19
33	213451_x_at	TNXA /// TNXB	tenascin XA (pseudogene) /// tenascin XB
34	242162_at	WDR69	WD repeat domain 69
35	242814_at	SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9
36	1569652_at	MLLT3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog,
37	228071_at	GIMAP7	GTPase, IMAP family member 7
38	211656_x_at	HLA-DQB1 /// LOC100	major histocompatibility complex, class II, DQ beta 1 /// HLA class
39	1562255_at	SYTL3	synaptotagmin-like 3
40	203996_s_at	C21orf2	chromosome 21 open reading frame 2
41	206011_at	CASP1	caspase 1, apoptosis-related cysteine peptidase
42	209785_s_at	PLA2G4C	phospholipase A2, group IVC (cytosolic, calcium-independent)
43	1559413_at	TCP11L2	t-complex 11 (mouse)-like 2
44	204103_at	CCL4	chemokine (C-C motif) ligand 4
45	214696_at	MIR22 /// MIR22HG	microRNA 22 /// MIR22 host gene (non-protein coding)
46	223504_at	DNAJC27	DnaJ (Hsp40) homolog, subfamily C, member 27
47	242916_at	CNTRL	centriolin

1	228903_at	CES4A	carboxylesterase 4A
2	212249_at	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)
3	229740_at	C17orf109	chromosome 17 open reading frame 109
4	220361_at	IQCH	IQ motif containing H
5	220102_at	FOXL2	forkhead box L2
6	206721_at	C1orf114	chromosome 1 open reading frame 114
7	213988_s_at	SAT1	spermidine/spermine N1-acetyltransferase 1
8	227148_at	PLEKHH2	pleckstrin homology domain containing, family H (with MyTH4 do
9	215078_at	LOC100129518	LOC100129518 // uncharacterized LOC100129518 // superoxide dismutase 2, mito
10	207330_at	PZP	pregnancy-zone protein
11	206496_at	FMO3	flavin containing monooxygenase 3
12	205902_at	KCNN3	potassium intermediate/small conductance calcium-activated cha
13	203973_s_at	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta
14	201952_at	ALCAM	activated leukocyte cell adhesion molecule
15	211006_s_at	KCNB1	potassium voltage-gated channel, Shab-related subfamily, membe
16	206417_at	CNGA1	cyclic nucleotide gated channel alpha 1
17	222549_at	CLDN1	claudin 1
18	203868_s_at	VCAM1	vascular cell adhesion molecule 1
19	213802_at	PRSS12	protease, serine, 12 (neutrotrypsin, motopsin)
20	206785_s_at	KLRC1 // KLRC2	killer cell lectin-like receptor subfamily C, member 1 // killer cell
21	230359_at	KNDC1	kinase non-catalytic C-lobe domain (KIND) containing 1
22	206374_at	DUSP8	dual specificity phosphatase 8
23	213568_at	OSR2	odd-skipped related 2 (Drosophila)
24	224590_at	XIST	X (inactive)-specific transcript (non-protein coding)
25	204440_at	CD83	CD83 molecule
26	221874_at	KIAA1324	KIAA1324
27	1554988_at	SLC9C2	solute carrier family 9, member C2 (putative)
28	206325_at	SERPINA6	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitry
29	206541_at	KLKB1	kalikrein B, plasma (Fletcher factor) 1
30	228097_at	MYLIP	myosin regulatory light chain interacting protein
31	209304_x_at	GADD45B	growth arrest and DNA-damage-inducible, beta
32	235946_at	RIBC1	RIB43A domain with coiled-coils 1
33	234732_s_at	EFCAB6	EF-hand calcium binding domain 6
34	227359_at	OSCP1	organic solute carrier partner 1
35	239213_at	SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1
36	215363_x_at	FOLH1 // FOLH1B	folate hydrolase (prostate-specific membrane antigen) 1 // folate
37	205922_at	VNN2	vanin 2
38	224568_x_at	LOC100507645	LOC100507645 // metastasis associated lung ad
39	1553605_a_at	ABCA13	ATP-binding cassette, sub-family A (ABC1), member 13
40	209687_at	CXCL12	chemokine (C-X-C motif) ligand 12
41	244144_at	SYNE1	spectrin repeat containing, nuclear envelope 1
42	1555298_a_at	VWA3B	von Willebrand factor A domain containing 3B
43	235649_at	ADAMTS8	ADAM metallopeptidase with thrombospondin type 1 motif, 8
44	229530_at	GUCY1A3	guanylate cyclase 1, soluble, alpha 3
45	224215_s_at	DLL1	delta-like 1 (Drosophila)
46	228128_x_at	PAPPA	pregnancy-associated plasma protein A, pappalysin 1
47	223794_at	ARMC4	armadillo repeat containing 4

1	213900_at	FAM189A2	family with sequence similarity 189, member A2
2	219290_x_at	DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides
3	235638_at	RASSF6	Ras association (RalGDS/AF-6) domain family member 6
4	228882_at	TUB	tubby homolog (mouse)
5	221834_at	LOC100507577	/// LOC100507577 /// ion peptidase 2, peroxisomal
6	1566480_x_at	C17orf104	Chromosome 17 open reading frame 104
7	244401_at	LCA5	Leber congenital amaurosis 5
8	239123_at	TSC22D1	TSC22 domain family, member 1
9	228532_at	C1orf162	chromosome 1 open reading frame 162
10	241359_at	TLCD2	TLC domain containing 2
11	213537_at	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1
12	219396_s_at	MIR631	/// NEIL1 microRNA 631 /// nei endonuclease VIII-like 1 (E. coli)
13	209879_at	SELPLG	selectin P ligand
14	215266_at	DNAH3	dynein, axonemal, heavy chain 3
15	201162_at	IGFBP7	insulin-like growth factor binding protein 7
16	213397_x_at	RNASE4	ribonuclease, RNase A family, 4
17	219014_at	PLAC8	placenta-specific 8
18	206093_x_at	TNXA	/// TNXB tenascin XA (pseudogene) /// tenascin XB
19	1562743_at	ZNF33B	zinc finger protein 33B
20	206710_s_at	EPB41L3	erythrocyte membrane protein band 4.1-like 3
21	236710_at	C1orf87	chromosome 1 open reading frame 87
22	1558792_x_at	AP2A1	Adaptor-related protein complex 2, alpha 1 subunit
23	243087_at	WDR63	WD repeat domain 63
24	230924_at	TTLL6	tubulin tyrosine ligase-like family, member 6
25	205383_s_at	ZBTB20	zinc finger and BTB domain containing 20
26	242290_at	TACC1	transforming, acidic coiled-coil containing protein 1
27	230378_at	SCGB3A1	secretoglobin, family 3A, member 1
28	230391_at	CD84	CD84 molecule
29	207808_s_at	PROS1	protein S (alpha)
30	237227_at	NEK10	NIMA (never in mitosis gene a)- related kinase 10
31	215322_at	LONRF1	LON peptidase N-terminal domain and ring finger 1
32	229233_at	NRG3	neuregulin 3
33	209447_at	SYNE1	spectrin repeat containing, nuclear envelope 1
34	1559400_s_at	PAPPA	pregnancy-associated plasma protein A, pappalysin 1
35	236331_at	CDKL2	cyclin-dependent kinase-like 2 (CDC2-related kinase)
36	1553183_at	UMODL1	uromodulin-like 1
37	218532_s_at	FAM134B	family with sequence similarity 134, member B
38	213309_at	PLCL2	phospholipase C-like 2
39	241193_at	ETS2	V-ets erythroblastosis virus E26 oncogene homolog 2 (avian)
40	1552321_a_at	CCDC65	coiled-coil domain containing 65
41	204487_s_at	KCNQ1	potassium voltage-gated channel, KQT-like subfamily, member 1
42	206017_at	KIAA0319	KIAA0319
43	219687_at	HHAT	hedgehog acyltransferase
44	229041_s_at	LOC100505746	uncharacterized LOC100505746
45	203924_at	GSTA1	glutathione S-transferase alpha 1
46	237719_x_at	RGS7BP	regulator of G-protein signaling 7 binding protein
47	223737_x_at	CHST9	carbohydrate (N-acetylgalactosamine 4-O) sulfotransferase 9

1	226917_s_at	ANAPC4	anaphase promoting complex subunit 4
2	216333_x_at	TNXA /// TNXB	tenascin XA (pseudogene) /// tenascin XB
3	227346_at	IKZF1	IKAROS family zinc finger 1 (Ikaros)
4	204894_s_at	AOC3	amine oxidase, copper containing 3 (vascular adhesion protein 1)
5	64900_at	TMEM231	transmembrane protein 231
6	216119_s_at	SPEF1	sperm flagellar 1
7	1552296_at	BEST4	bestrophin 4
8	221698_s_at	CLEC7A	C-type lectin domain family 7, member A
9	206483_at	LRRC6	leucine rich repeat containing 6
10	206101_at	ECM2	extracellular matrix protein 2, female organ and adipocyte specific
11	211621_at	AR	androgen receptor
12	204655_at	CCL5	chemokine (C-C motif) ligand 5
13	1554919_s_at	C7orf63	chromosome 7 open reading frame 63
14	239336_at	THBS1	thrombospondin 1
15	213185_at	KIAA0556	KIAA0556
16	230287_at	SGSM1	small G protein signaling modulator 1
17	231728_at	CAPS	calcyphosine
18	223732_at	SLC23A1	solute carrier family 23 (nucleobase transporters), member 1
19	217362_x_at	HLA-DRB6	major histocompatibility complex, class II, DR beta 6 (pseudogene)
20	238423_at	SYTL3	synaptotagmin-like 3
21	209606_at	CYTIP	cytohesin 1 interacting protein
22	243868_at	RFX3	regulatory factor X, 3 (influences HLA class II expression)
23	226872_at	RFX2	regulatory factor X, 2 (influences HLA class II expression)
24	232617_at	CTSS	cathepsin S
25	224916_at	TMEM173	transmembrane protein 173
26	219371_s_at	KLF2	Kruppel-like factor 2 (lung)
27	233312_at	ROPN1L	rhophilin associated tail protein 1-like
28	209114_at	TSPAN1	tetraspanin 1
29	219734_at	SIDT1	SID1 transmembrane family, member 1
30	219455_at	C7orf63	chromosome 7 open reading frame 63
31	215418_at	PARVA	parvin, alpha
32	1405_i_at	CCL5	chemokine (C-C motif) ligand 5
33	234476_at	DNAH7	dynein, axonemal, heavy chain 7
34	1552957_at	DNAH6	dynein, axonemal, heavy chain 6
35	202158_s_at	CELF2	CUGBP, Elav-like family member 2
36	243334_at	CACNA1D	calcium channel, voltage-dependent, L type, alpha 1D subunit
37	209173_at	AGR2	anterior gradient 2 homolog (Xenopus laevis)
38	1553789_a_at	C21orf58	chromosome 21 open reading frame 58
39	237238_at	WWC1	WW and C2 domain containing 1
40	225941_at	EIF4E3	eukaryotic translation initiation factor 4E family member 3
41	205114_s_at	CCL3 /// CCL3L1 /// CC	chemokine (C-C motif) ligand 3 /// chemokine (C-C motif) ligand 3
42	1560397_s_at	KLHL6	kelch-like 6 (Drosophila)
43	242342_at	GUCY1A2	guanylate cyclase 1, soluble, alpha 2
44	238763_at	RBM20	RNA binding motif protein 20
45	1568906_at	LOC728196	uncharacterized LOC728196
46	237251_at	LRRC71	leucine rich repeat containing 71
47	242286_at	GRIN2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A

1	205890_s_at	GABBR1 /// UBD	gamma-aminobutyric acid (GABA) B receptor, 1 /// ubiquitin D
2	211726_s_at	FMO2	flavin containing monooxygenase 2 (non-functional)
3	222102_at	GSTA3	glutathione S-transferase alpha 3
4	228086_at	STK33	serine/threonine kinase 33
5	210136_at	MBP	myelin basic protein
6	228111_s_at	DNAH1	dynein, axonemal, heavy chain 1
7	220173_at	C14orf45	chromosome 14 open reading frame 45
8	213385_at	CHN2	chimerin (chimaerin) 2
9	222858_s_at	DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides
10	220308_at	CCDC19	coiled-coil domain containing 19
11	207651_at	GPR171	G protein-coupled receptor 171
12	243495_s_at	ZNF652	Zinc finger protein 652
13	230807_at	CCDC151	coiled-coil domain containing 151
14	211896_s_at	DCN	decorin
15	226218_at	IL7R	interleukin 7 receptor
16	233463_at	RASSF6	Ras association (RalGDS/AF-6) domain family member 6
17	206043_s_at	ATP2C2	ATPase, Ca++ transporting, type 2C, member 2
18	220475_at	SLC28A3	solute carrier family 28 (sodium-coupled nucleoside transporter), glucosaminyl (N-acetyl) transferase 3, mucin type
19	219508_at	GCNT3	KIAA1324
20	226248_s_at	KIAA1324	protocadherin beta 16
21	232099_at	PCDHB16	MAM domain containing 2
22	228885_at	MAMDC2	kelch repeat and BTB (POZ) domain containing 10
23	219106_s_at	KBTBD10	nicotinamide riboside kinase 1
24	219147_s_at	NMRK1	LOC100506124 /// TT(uncharacterized LOC100506124 /// tetratricopeptide repeat domain
25	220064_at	LOC100506124	membrane-spanning 4-domains, subfamily A, member 7
26	223343_at	MS4A7	major histocompatibility complex, class II, DO alpha
27	226878_at	HLA-DOA	solute carrier family 22 (organic cation/ergothioneine transporter
28	205896_at	SLC22A4	EF-hand calcium binding domain 6
29	1562815_at	EFCAB6	defensin, beta 124
30	1568377_x_at	DEFB124	glucosidase, beta, acid 3 (cytosolic)
31	222943_at	GBA3	Kruppel-like factor 9
32	203542_s_at	KLF9	leucine rich repeat containing 43
33	1553729_s_at	LRRC43	zinc finger, MYND-type containing 12
34	223636_at	ZMYND12	activated leukocyte cell adhesion molecule
35	201951_at	ALCAM	myosin VB
36	225299_at	MYO5B	chromosome 2 open reading frame 50
37	1563814_at	C2orf50	RSPH10B /// RSPH10B radial spoke head 10 homolog B (Chlamydomonas) /// radial spok
38	1557417_s_at	RSPH10B	protocadherin 17
39	205656_at	PCDH17	SHC (Src homology 2 domain containing) transforming protein 2
40	213464_at	SHC2	ATPase, Ca++ transporting, type 2C, member 2
41	214798_at	ATP2C2	microtubule-associated protein 6
42	228943_at	MAP6	chromosome 9 open reading frame 72
43	1553133_at	C9orf72	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitry
44	202376_at	SERPINA3	pleckstrin homology domain containing, family A member 6
45	229245_at	PLEKHA6	dynein, axonemal, assembly factor 3
46	230033_at	DNAAF3	vanin 3
47	220528_at	VNN3	

1	233198_at	GOLGA2P5	golgin A2 pseudogene 5
2	237439_at	USP43	ubiquitin specific peptidase 43
3	224941_at	PAPPA	pregnancy-associated plasma protein A, pappalysin 1
4	219857_at	PLEKHS1	pleckstrin homology domain containing, family S member 1
5	210592_s_at	SAT1	spermidine/spermine N1-acetyltransferase 1
6	205654_at	C4BPA	complement component 4 binding protein, alpha
7	234974_at	GALM	galactose mutarotase (aldose 1-epimerase)
8	225207_at	PDK4	pyruvate dehydrogenase kinase, isozyme 4
9	227775_at	CELF6	CUGBP, Elav-like family member 6
10	236407_at	KCNE1	potassium voltage-gated channel, Isk-related family, member 1
11	227474_at	LOC654433	uncharacterized LOC654433
12	1560147_at	WDR86-AS1	WDR86 antisense RNA 1 (non-protein coding)
13	212451_at	SECISBP2L	SECIS binding protein 2-like
14	227226_at	MRAP2	melanocortin 2 receptor accessory protein 2
15	230499_at	BIRC3	baculoviral IAP repeat containing 3
16	238720_at	LOC100506582	uncharacterized LOC100506582
17	201743_at	CD14	CD14 molecule
18	1552540_s_at	IQCD	IQ motif containing D
19	237363_at	SPATA6L	spermatogenesis associated 6-like
20	214735_at	IPCEF1	interaction protein for cytohesin exchange factors 1
21	212188_at	KCTD12	potassium channel tetramerisation domain containing 12
22	202643_s_at	TNFAIP3	tumor necrosis factor, alpha-induced protein 3
23	227812_at	TNFRSF19	tumor necrosis factor receptor superfamily, member 19
24	201497_x_at	MYH11	myosin, heavy chain 11, smooth muscle
25	220724_at	CWH43	cell wall biogenesis 43 C-terminal homolog (S. cerevisiae)
26	231149_s_at	ULK4	unc-51-like kinase 4 (C. elegans)
27	205945_at	IL6R	interleukin 6 receptor
28	201289_at	CYR61	cysteine-rich, angiogenic inducer, 61
29	235308_at	ZBTB20	zinc finger and BTB domain containing 20
30	228946_at	INTU	inturned planar cell polarity effector homolog (Drosophila)
31	205714_s_at	ZMYND10	zinc finger, MYND-type containing 10
32	212327_at	LIMCH1	LIM and calponin homology domains 1
33	205044_at	GABRP	gamma-aminobutyric acid (GABA) A receptor, pi
34	230828_at	GRAMD2	GRAM domain containing 2
35	202435_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1
36	1564160_at	DTHD1	death domain containing 1
37	238721_at	MDH1B	malate dehydrogenase 1B, NAD (soluble)
38	236293_at	RHOH	ras homolog family member H
39	230451_at	LOC100506974	uncharacterized LOC100506974
40	2422287_at	CLIP1	CAP-GLY domain containing linker protein 1
41	228221_at	SLC44A3	solute carrier family 44, member 3
42	235213_at	ITPKB	Inositol-trisphosphate 3-kinase B
43	232449_at	BCO2	beta-carotene oxygenase 2
44	207992_s_at	AMPD3	adenosine monophosphate deaminase 3
45	226822_at	STOX2	storkhead box 2
46	226690_at	ADCYAP1R1	adenylate cyclase activating polypeptide 1 (pituitary) receptor typ
47	230505_at	LOC145474	uncharacterized LOC145474

1	232972_at	C17orf72	chromosome 17 open reading frame 72
2	220920_at	ATP10B	ATPase, class V, type 10B
3	224209_s_at	GDA	guanine deaminase
4	205898_at	CX3CR1	chemokine (C-X3-C motif) receptor 1
5	205288_at	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)
6	214261_s_at	ADH6	alcohol dehydrogenase 6 (class V)
7	229849_at	WIPF3	WAS/WASL interacting protein family, member 3
8	230273_at	C6orf165	chromosome 6 open reading frame 165
9	224559_at	LOC100507645	uncharacterized LOC100507645 /// metastasis associated lung ad
10	223217_s_at	NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells
11	204793_at	GPRASP1	G protein-coupled receptor associated sorting protein 1
12	233375_at	EFCAB2	EF-hand calcium binding domain 2
13	223623_at	C2orf40	chromosome 2 open reading frame 40
14	200810_s_at	CIRBP	cold inducible RNA binding protein
15	232417_x_at	ZDHHC11	zinc finger, DHHC-type containing 11
16	230092_at	UBXN10	UBX domain protein 10
17	232611_at	GOLGA2P5	golgin A2 pseudogene 5
18	228214_at	SOX6	SRY (sex determining region Y)-box 6
19	1556474_a_at	FLJ38379	uncharacterized FLJ38379
20	238008_at	PRR18	proline rich 18
21	1556421_at	LOC286189	uncharacterized LOC286189
22	238657_at	UBXN10	UBX domain protein 10
23	228338_at	C11orf93	chromosome 11 open reading frame 93
24	204714_s_at	F5	coagulation factor V (proaccelerin, labile factor)
25	204070_at	RARRES3	retinoic acid receptor responder (tazarotene induced) 3
26	235945_at	SRD5A2	Steroid-5-alpha-reductase, alpha polypeptide 2 (3-oxo-5 alpha-ste
27	230132_at	LOC100505495	uncharacterized LOC100505495
28	210742_at	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)
29	205923_at	RELN	reelin
30	202746_at	ITM2A	integral membrane protein 2A
31	207981_s_at	ESRRG	estrogen-related receptor gamma
32	227289_at	PCDH17	protocadherin 17
33	208131_s_at	PTGIS	prostaglandin I2 (prostacyclin) synthase
34	244655_at	LOC100507311	uncharacterized LOC100507311
35	203932_at	HLA-DMB	major histocompatibility complex, class II, DM beta
36	204365_s_at	REEP1	receptor accessory protein 1
37	223218_s_at	NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells
38	211368_s_at	CASP1	caspase 1, apoptosis-related cysteine peptidase
39	220184_at	NANOG	Nanog homeobox
40	235421_at	MAP3K8	mitogen-activated protein kinase kinase kinase 8
41	205249_at	EGR2	early growth response 2
42	231133_at	CCDC164	coiled-coil domain containing 164
43	238513_at	PRRG4	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)
44	215341_at	DNAH6	dynein, axonemal, heavy chain 6
45	235746_s_at	PLA2R1	phospholipase A2 receptor 1, 180kDa
46	214414_x_at	HBA1 /// HBA2	hemoglobin, alpha 1 /// hemoglobin, alpha 2
47	232196_at	LCA5L	Leber congenital amaurosis 5-like

1	217478_s_at	HLA-DMA	major histocompatibility complex, class II, DM alpha
2	214889_at	FAM149A	family with sequence similarity 149, member A
3	223866_at	ARMC2	armadillo repeat containing 2
4	218510_x_at	FAM134B	family with sequence similarity 134, member B
5	205269_at	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte
6	40665_at	FMO3	flavin containing monooxygenase 3
7	228325_at	KIAA0146	KIAA0146
8	224940_s_at	PAPPA	pregnancy-associated plasma protein A, pappalysin 1
9	1568606_at	C11orf88	chromosome 11 open reading frame 88
10	228503_at	RPS6KA6	ribosomal protein S6 kinase, 90kDa, polypeptide 6
11	211458_s_at	GABARAPL1 /// GABA(A) receptor-associated protein like 1 /// GABA(A) receptors	GABA(A) receptor-associated protein like 1 /// GABA(A) receptors
12	226358_at	APH1B	anterior pharynx defective 1 homolog B (<i>C. elegans</i>)
13	202156_s_at	CELF2	CUGBP, Elav-like family member 2
14	212914_at	CBX7	chromobox homolog 7
15	1568698_at	TMEM232	transmembrane protein 232
16	227404_s_at	LOC100653132	uncharacterized LOC100653132
17	229918_at	CCDC40	coiled-coil domain containing 40
18	239722_at	C5orf49	chromosome 5 open reading frame 49
19	228035_at	STK33	serine/threonine kinase 33
20	225345_s_at	FBXO32	F-box protein 32
21	229147_at	RASSF6	Ras association (RalGDS/AF-6) domain family member 6
22	220232_at	SCD5	stearoyl-CoA desaturase 5
23	203131_at	PDGFRA	platelet-derived growth factor receptor, alpha polypeptide
24	239098_at	KCNRG	potassium channel regulator
25	205997_at	ADAM28	ADAM metallopeptidase domain 28
26	219833_s_at	EFHC1	EF-hand domain (C-terminal) containing 1
27	214890_s_at	FAM149A	family with sequence similarity 149, member A
28	236575_at	ARHGEF26-AS1	ARHGEF26 antisense RNA 1 (non-protein coding)
29	231044_at	C1orf194	chromosome 1 open reading frame 194
30	239921_at	COL28A1	collagen, type XXVIII, alpha 1
31	239185_at	ABCA9	ATP-binding cassette, sub-family A (ABC1), member 9
32	231565_at	C4orf22	chromosome 4 open reading frame 22
33	203455_s_at	SAT1	spermidine/spermine N1-acetyltransferase 1
34	240288_at	KCNRG /// TRIM13	potassium channel regulator /// tripartite motif containing 13
35	1554141_s_at	WDR78	WD repeat domain 78
36	227420_at	TNFAIP8L1	tumor necrosis factor, alpha-induced protein 8-like 1
37	225009_at	CMTM4	CKLF-like MARVEL transmembrane domain containing 4
38	230104_s_at	TPPP	tubulin polymerization promoting protein
39	241600_at	WIPF3	WAS/WASL interacting protein family, member 3
40	226439_s_at	NBEA	neurobeachin
41	228195_at	C2orf88	chromosome 2 open reading frame 88
42	226333_at	IL6R	interleukin 6 receptor
43	226778_at	C8orf42	chromosome 8 open reading frame 42
44	228546_at	DPP6	dipeptidyl-peptidase 6
45	223609_at	ROPN1L	rhophilin associated tail protein 1-like
46	236335_at	GUCY1A2	guanylate cyclase 1, soluble, alpha 2
47	239828_at	AKD1	adenylate kinase domain containing 1

1	209959_at	NR4A3	nuclear receptor subfamily 4, group A, member 3
2	205363_at	BBOX1	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-but
3	220156_at	EFCAB1	EF-hand calcium binding domain 1
4	231710_at	CAPS	calcypbosine
5	209160_at	AKR1C3	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid
6	243296_at	NAMPT	Nicotinamide phosphoribosyltransferase
7	233071_at	RSPH4A	radial spoke head 4 homolog A (Chlamydomonas)
8	1552365_at	SCIN	scinderin
9	202901_x_at	CTSS	cathepsin S
10	230792_at	FAAH2	fatty acid amide hydrolase 2
11	227088_at	PDE5A	phosphodiesterase 5A, cGMP-specific
12	1553794_at	STOML3	stomatin (EPB72)-like 3
13	230206_at	DOCK5	Dedicator of cytokinesis 5
14	238864_at	VWA3A	von Willebrand factor A domain containing 3A
15	225286_at	ARSD	arylsulfatase D
16	220125_at	DNAI1	dynein, axonemal, intermediate chain 1
17	220030_at	STYK1	serine/threonine/tyrosine kinase 1
18	200974_at	ACTA2	actin, alpha 2, smooth muscle, aorta
19	202340_x_at	NR4A1	nuclear receptor subfamily 4, group A, member 1
20	219511_s_at	SNCAIP	synuclein, alpha interacting protein
21	209795_at	CD69	CD69 molecule
22	1569675_at	POU2AF1	POU class 2 associating factor 1
23	1555804_a_at	YSK4	YSK4 Sps1/Ste20-related kinase homolog (S. cerevisiae)
24	209071_s_at	RGS5	regulator of G-protein signaling 5
25	213172_at	TTC9	tetratricopeptide repeat domain 9
26	227758_at	RERG	RAS-like, estrogen-regulated, growth inhibitor
27	239500_at	EFCAB1	EF-hand calcium binding domain 1
28	207996_s_at	C18orf1	chromosome 18 open reading frame 1
29	220389_at	CCDC81	coiled-coil domain containing 81
30	240809_at	ZNF295-AS1	ZNF295 antisense RNA 1 (non-protein coding)
31	215085_x_at	DLEC1	deleted in lung and esophageal cancer 1
32	207655_s_at	BLNK	B-cell linker
33	243036_at	CCDC30	coiled-coil domain containing 30
34	219681_s_at	RAB11FIP1	RAB11 family interacting protein 1 (class I)
35	219747_at	NDNF	neuron-derived neurotrophic factor
36	229628_s_at	C9orf174 /// LOC1004 chromsome 9 open reading frame 174 /// LOC100499484-C9orf:	
37	209074_s_at	FAM107A /// LOC100499484-C9orf:	family with sequence similarity 107, member A /// uncharacterized
38	224227_s_at	BDP1	B double prime 1, subunit of RNA polymerase III transcription initiation
39	221103_s_at	WDR52	WD repeat domain 52
40	1557544_at	CCDC147	coiled-coil domain containing 147
41	1552733_at	KLHDC1	kelch domain containing 1
42	212999_x_at	HLA-DQB1 /// LOC100499484-C9orf:	major histocompatibility complex, class II, DQ beta 1 /// HLA class II
43	224929_at	TMEM173	transmembrane protein 173
44	203029_s_at	PTPRN2	protein tyrosine phosphatase, receptor type, N polypeptide 2
45	237131_at	RIIAD1	regulatory subunit of type II PKA R-subunit (RIIa) domain containing 1
46	231389_at	CXorf41	chromosome X open reading frame 41
47	206385_s_at	ANK3	ankyrin 3, node of Ranvier (ankyrin G)

1	1554528_at	C3orf15 /// LOC10065 chromosome 3 open reading frame 15 /// uncharacterized LOC10
2	204621_s_at	NR4A2 nuclear receptor subfamily 4, group A, member 2
3	223867_at	TEKT3 tektin 3
4	210108_at	CACNA1D calcium channel, voltage-dependent, L type, alpha 1D subunit
5	241365_at	SATB1 SATB homeobox 1
6	220623_s_at	TSGA10 testis specific, 10
7	237151_s_at	PCDP1 primary ciliary dyskinesia protein 1
8	205768_s_at	SLC27A2 solute carrier family 27 (fatty acid transporter), member 2
9	214234_s_at	CYP3A5 cytochrome P450, family 3, subfamily A, polypeptide 5
10	212587_s_at	PTPRC protein tyrosine phosphatase, receptor type, C
11	202994_s_at	FBLN1 fibulin 1
12	1554547_at	FAM13C family with sequence similarity 13, member C
13	1552594_at	TMEM190 transmembrane protein 190
14	207850_at	CXCL3 chemokine (C-X-C motif) ligand 3
15	213375_s_at	N4BP2L1 NEDD4 binding protein 2-like 1
16	229021_at	MCTP2 multiple C2 domains, transmembrane 2
17	210033_s_at	SPAG6 sperm associated antigen 6
18	203408_s_at	SATB1 SATB homeobox 1
19	214070_s_at	ATP10B ATPase, class V, type 10B
20	214719_at	SLC46A3 solute carrier family 46, member 3
21	201859_at	SRGN serglycin
22	1553734_at	AK7 adenylate kinase 7
23	232357_at	TTLL9 tubulin tyrosine ligase-like family, member 9
24	214823_at	ZNF204P zinc finger protein 204, pseudogene
25	223695_s_at	ARSD arylsulfatase D
26	220351_at	CCRL1 chemokine (C-C motif) receptor-like 1
27	207636_at	SERPNI2 serpin peptidase inhibitor, clade I (pancpin), member 2
28	239776_at	TMEM232 transmembrane protein 232
29	1567627_at	CD74 CD74 molecule, major histocompatibility complex, class II invariant
30	214222_at	DNAH7 dynein, axonemal, heavy chain 7
31	228806_at	RORC RAR-related orphan receptor C
32	237314_at	ENKUR enkurin, TRPC channel interacting protein
33	243900_at	WDR38 WD repeat domain 38
34	222592_s_at	ACSL5 acyl-CoA synthetase long-chain family member 5
35	219542_at	NEK11 NIMA (never in mitosis gene a)- related kinase 11
36	207547_s_at	FAM107A /// LOC10065 family with sequence similarity 107, member A /// uncharacterized
37	203240_at	FCGBP Fc fragment of IgG binding protein
38	230454_at	ICA1L islet cell autoantigen 1,69kDa-like
39	212224_at	ALDH1A1 aldehyde dehydrogenase 1 family, member A1
40	1556711_at	FAM216B family with sequence similarity 216, member B
41	204748_at	PTGS2 prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase)
42	205769_at	SLC27A2 solute carrier family 27 (fatty acid transporter), member 2
43	227497_at	SOX6 SRY (sex determining region Y)-box 6
44	236915_at	C4orf47 chromosome 4 open reading frame 47
45	221841_s_at	KLF4 Kruppel-like factor 4 (gut)
46	235956_at	KIAA1377 KIAA1377
47	1557275_a_at	TLCD2 TLC domain containing 2

1	230131_x_at	ARSD	arylsulfatase D
2	201236_s_at	BTG2	BTG family, member 2
3	225919_s_at	C9orf72	chromosome 9 open reading frame 72
4	238049_at	GRAMD3	GRAM domain containing 3
5	223691_at	RGS22	regulator of G-protein signaling 22
6	1557867_s_at	C9orf117	chromosome 9 open reading frame 117
7	203824_at	TSPAN8	tetraspanin 8
8	230997_at	TTC21A	tetratricopeptide repeat domain 21A
9	232568_at	MGC24103	uncharacterized MGC24103
10	1558077_s_at	MDH1B	malate dehydrogenase 1B, NAD (soluble)
11	223823_at	KCNMB2	potassium large conductance calcium-activated channel, subfamily
12	224370_s_at	CAPS2	calcyphosine 2
13	201041_s_at	DUSP1	dual specificity phosphatase 1
14	1559640_at	ANKFN1	Ankyrin-repeat and fibronectin type III domain containing 1
15	223467_at	RASD1	RAS, dexamethasone-induced 1
16	212067_s_at	C1R	complement component 1, r subcomponent
17	206197_at	NME5	NME/NM23 family member 5
18	213661_at	PAMR1	peptidase domain containing associated with muscle regeneration
19	206798_x_at	DLEC1	deleted in lung and esophageal cancer 1
20	210982_s_at	HLA-DRA	major histocompatibility complex, class II, DR alpha
21	218380_at	LOC728392	uncharacterized LOC728392
22	205844_at	VNN1	vanin 1
23	222722_at	OGN	osteoglycin
24	201893_x_at	DCN	decorin
25	220302_at	MAK	male germ cell-associated kinase
26	242904_x_at	LOC100653229	uncharacterized LOC100653229
27	228731_at	GUCY1A2	guanylate cyclase 1, soluble, alpha 2
28	241538_at	CXorf30	chromosome X open reading frame 30
29	230695_s_at	RSPH9	radial spoke head 9 homolog (Chlamydomonas)
30	217757_at	A2M	alpha-2-macroglobulin
31	210809_s_at	POSTN	periostin, osteoblast specific factor
32	208894_at	HLA-DRA	major histocompatibility complex, class II, DR alpha
33	201137_s_at	HLA-DPB1	major histocompatibility complex, class II, DP beta 1
34	228827_at	RUNX1T1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)
35	223475_at	CRISPLD1	cysteine-rich secretory protein LCCL domain containing 1
36	1556003_a_at	LOC100506777	uncharacterized LOC100506777
37	200878_at	EPAS1 /// LOC1006521	endothelial PAS domain protein 1 /// uncharacterized LOC1006521
38	205590_at	RASGRP1	RAS guanyl releasing protein 1 (calcium and DAG-regulated)
39	236430_at	TMED6	transmembrane emp24 protein transport domain containing 6
40	221646_s_at	ZDHHC11	zinc finger, DHHC-type containing 11
41	221667_s_at	HSPB8	heat shock 22kDa protein 8
42	225280_x_at	ARSD	arylsulfatase D
43	233011_at	ANXA1	Annexin A1
44	237020_at	CATSPERD	catSPER channel auxiliary subunit delta
45	202437_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1
46	226164_x_at	RIMKLB	ribosomal modification protein rimK-like family member B
47	205414_s_at	ARHGAP44	Rho GTPase activating protein 44

1	242903_at	IFNGR1	interferon gamma receptor 1
2	232166_at	KIAA1377	KIAA1377
3	239216_at	TEKT1	tektin 1
4	212671_s_at	HLA-DQA1	/// HLA-DQ major histocompatibility complex, class II, DQ alpha 1
5			/// major histocompatibility complex, class II, DQ alpha 1
6	204041_at	MAOB	monoamine oxidase B
7	216248_s_at	NR4A2	nuclear receptor subfamily 4, group A, member 2
8	206228_at	PAX2	paired box 2
9	212998_x_at	HLA-DQB1	/// LOC100 major histocompatibility complex, class II, DQ beta 1
10			/// HLA class II, DQ beta 1
11	219505_at	CECR1	cat eye syndrome chromosome region, candidate 1
12	240293_at	CCDC153	coiled-coil domain containing 153
13	229096_at	LIMS3	/// LIMS3-LOC4 LIM and senescent cell antigen-like domains 3
14			/// LIMS3-LOC4 LIM and senescent cell antigen-like domains 3
15	227194_at	FAM3B	family with sequence similarity 3, member B
16	230193_at	WDR66	WD repeat domain 66
17	243109_at	MCTP2	multiple C2 domains, transmembrane 2
18	230152_at	WDR52	WD repeat domain 52
19	202295_s_at	CTSH	cathepsin H
20	207959_s_at	DNAH9	dynein, axonemal, heavy chain 9
21	213849_s_at	PPP2R2B	protein phosphatase 2, regulatory subunit B, beta
22	207574_s_at	GADD45B	growth arrest and DNA-damage-inducible, beta
23	228648_at	LRG1	leucine-rich alpha-2-glycoprotein 1
24	228482_at	CDRT4	/// FAM18B2-CCMT1A duplicated region transcript 4
25			/// FAM18B2-CDRT4 readthrough
26	235086_at	THBS1	thrombospondin 1
27	230130_at	SLIT2	Slit homolog 2 (Drosophila)
28	205043_at	CFTR	cystic fibrosis transmembrane conductance regulator (ATP-bindin
29	236666_s_at	LRRC10B	leucine rich repeat containing 10B
30	204622_x_at	NR4A2	nuclear receptor subfamily 4, group A, member 2
31	227917_at	LOC100506990	uncharacterized LOC100506990
32	220168_at	CASC1	cancer susceptibility candidate 1
33	209550_at	NDN	necdin homolog (mouse)
34	204803_s_at	RRAD	Ras-related associated with diabetes
35	226682_at	RORA	RAR-related orphan receptor A
36	239499_at	DNAH2	dynein, axonemal, heavy chain 2
37	222068_s_at	DNAAF1	dynein, axonemal, assembly factor 1
38	225895_at	SYNPO2	synaptopodin 2
39	214204_at	PACRG	PARK2 co-regulated
40	212681_at	EPB41L3	erythrocyte membrane protein band 4.1-like 3
41	238327_at	ODF3B	outer dense fiber of sperm tails 3B
42	1554140_at	WDR78	WD repeat domain 78
43	239733_at	DYDC2	DPY30 domain containing 2
44	213975_s_at	LYZ	lysozyme
45	222162_s_at	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1
46	235527_at	DLGAP1	discs, large (Drosophila) homolog-associated protein 1
47	229976_at	MORN5	MORN repeat containing 5
48	243803_at	LOC643037	uncharacterized LOC643037
49	207896_s_at	DLEC1	deleted in lung and esophageal cancer 1
50	219564_at	KCNJ16	potassium inwardly-rectifying channel, subfamily J, member 16
51	222291_at	FAM149A	family with sequence similarity 149, member A

1	204072_s_at	FRY	furry homolog (Drosophila)
2	236118_at	LOC100128893	uncharacterized LOC100128893
3	226197_at	AR	androgen receptor
4	220591_s_at	EFHC2	EF-hand domain (C-terminal) containing 2
5	229802_at	WISP1	WNT1 inducible signaling pathway protein 1
6	238805_at	C11orf52 /// HSPB2 // chromosome 11 open reading frame 52 /// heat shock 27kDa prot	
7	221541_at	CRISPLD2	cysteine-rich secretory protein LCCL domain containing 2
8	1556026_at	LOC100131434	uncharacterized LOC100131434
9	231172_at	C9orf117	chromosome 9 open reading frame 117
10	202644_s_at	TNFAIP3	tumor necrosis factor, alpha-induced protein 3
11	238682_at	CCDC96	coiled-coil domain containing 96
12	203685_at	BCL2	B-cell CLL/lymphoma 2
13	234970_at	TC2N	tandem C2 domains, nuclear
14	243386_at	CASZ1	castor zinc finger 1
15	208147_s_at	CYP2C8	cytochrome P450, family 2, subfamily C, polypeptide 8
16	232968_at	FANK1	fibronectin type III and ankyrin repeat domains 1
17	218353_at	RGS5	regulator of G-protein signaling 5
18	236203_at	HLA-DQA1 /// LOC100	major histocompatibility complex, class II, DQ alpha 1 /// HLA clas
19	219871_at	FLJ13197	uncharacterized FLJ13197
20	237654_at	PPP1R36	protein phosphatase 1, regulatory subunit 36
21	204364_s_at	REEP1	receptor accessory protein 1
22	229738_at	DNAH10	dynein, axonemal, heavy chain 10
23	208323_s_at	ANXA13	annexin A13
24	231380_at	C8orf34	chromosome 8 open reading frame 34
25	232603_at	DCDC5	doublecortin domain containing 5
26	230624_at	SLC25A27	solute carrier family 25, member 27
27	208140_s_at	LRRC48	leucine rich repeat containing 48
28	205765_at	CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5
29	1569040_s_at	ANKRD36BP2	ankyrin repeat domain 36B pseudogene 2
30	228726_at	SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1
31	207490_at	TUBA4B	tubulin, alpha 4b (pseudogene)
32	212805_at	PRUNE2	prune homolog 2 (Drosophila)
33	201531_at	ZFP36	zinc finger protein 36, C3H type, homolog (mouse)
34	231729_s_at	CAPS	calcyphosine
35	230323_s_at	TMEM45B	transmembrane protein 45B
36	219932_at	SLC27A6	solute carrier family 27 (fatty acid transporter), member 6
37	227091_at	CCDC146	coiled-coil domain containing 146
38	210002_at	GATA6	GATA binding protein 6
39	205432_at	OVGP1	oviductal glycoprotein 1, 120kDa
40	226147_s_at	PIGR	polymeric immunoglobulin receptor
41	220723_s_at	CWH43	cell wall biogenesis 43 C-terminal homolog (S. cerevisiae)
42	203413_at	LOC100653018 /// LO	uncharacterized LOC100653018 /// uncharacterized LOC10065321
43	232381_s_at	DNAH5	dynein, axonemal, heavy chain 5
44	227697_at	SOCS3	suppressor of cytokine signaling 3
45	227498_at	SOX6	SRY (sex determining region Y)-box 6
46	227742_at	CLIC6	chloride intracellular channel 6
47	218876_at	TPPP3	tubulin polymerization-promoting protein family member 3

1	229616_s_at	GRAMD2	GRAM domain containing 2
2	204051_s_at	SFRP4	secreted frizzled-related protein 4
3	208306_x_at	HLA-DRB1 /// LOC100161961	major histocompatibility complex, class II, DR beta 1 /// HLA class
4	213293_s_at	TRIM22	tripartite motif containing 22
5	1552390_a_at	C8orf47	chromosome 8 open reading frame 47
6	232984_at	HYDIN	HYDIN, axonemal central pair apparatus protein
7	214235_at	CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5
8	1557636_a_at	C7orf57	chromosome 7 open reading frame 57
9	226192_at	AR	androgen receptor
10	208791_at	CLU	clusterin
11	239297_at	KIAA1456	KIAA1456
12	1554298_a_at	WDR49	WD repeat domain 49
13	218322_s_at	ACSL5	acyl-CoA synthetase long-chain family member 5
14	240857_at	DNAH9	dynein, axonemal, heavy chain 9
15	203780_at	MPZL2	myelin protein zero-like 2
16	223962_at	TTC29	tetratricopeptide repeat domain 29
17	39248_at	AQP3	aquaporin 3 (Gill blood group)
18	1552283_s_at	ZDHHC11	zinc finger, DHHC-type containing 11
19	223235_s_at	SMOC2	SPARC related modular calcium binding 2
20	204802_at	RRAD	Ras-related associated with diabetes
21	213308_at	SHANK2	SH3 and multiple ankyrin repeat domains 2
22	236909_at	C2orf77	chromosome 2 open reading frame 77
23	235650_at	CDHR3 /// LOC100652	cadherin-related family member 3 /// uncharacterized LOC100652
24	210323_at	TEKT2	tektin 2 (testicular)
25	237281_at	AKAP14	A kinase (PRKA) anchor protein 14
26	206815_at	SPAG8	sperm associated antigen 8
27	236320_at	CCDC17	coiled-coil domain containing 17
28	220636_at	DNAI2	dynein, axonemal, intermediate chain 2
29	200986_at	SERPING1	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1
30	209189_at	FOS	FBJ murine osteosarcoma viral oncogene homolog
31	230601_s_at	LRRC46	leucine rich repeat containing 46
32	228167_at	KLHL6	kelch-like 6 (Drosophila)
33	227238_at	MUC15	mucin 15, cell surface associated
34	239477_at	EFHB	EF-hand domain family, member B
35	204670_x_at	HLA-DRB1 /// HLA-DRB1	major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 1
36	208096_s_at	COL21A1	collagen, type XXI, alpha 1
37	209335_at	DCN	decorin
38	230600_at	LRRC46	leucine rich repeat containing 46
39	213307_at	SHANK2	SH3 and multiple ankyrin repeat domains 2
40	209774_x_at	CXCL2	chemokine (C-X-C motif) ligand 2
41	231582_at	CDHR3 /// LOC100652	cadherin-related family member 3 /// uncharacterized LOC100652
42	224355_s_at	MS4A8B	membrane-spanning 4-domains, subfamily A, member 8B
43	207016_s_at	ALDH1A2	aldehyde dehydrogenase 1 family, member A2
44	209312_x_at	HLA-DRB1 /// HLA-DRB1	major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 1
45	222043_at	CLU	clusterin
46	232277_at	SLC28A3	solute carrier family 28 (sodium-coupled nucleoside transporter),
47	209392_at	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2

1	228067_at	C2orf55	chromosome 2 open reading frame 55
2	208268_at	ADAM28	ADAM metallopeptidase domain 28
3	231969_at	STOX2	storkhead box 2
4	236717_at	FAM179A	family with sequence similarity 179, member A
5	205709_s_at	CDS1	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) :
6	228100_at	C1orf88	chromosome 1 open reading frame 88
7	219580_s_at	TMC5	transmembrane channel-like 5
8	226424_at	CAPS	calcypohosine
9	203485_at	RTN1	reticulon 1
10	1553635_s_at	TCTEX1D1	Tctex1 domain containing 1
11	226185_at	CDS1	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) :
12	243681_at	SHANK2	SH3 and multiple ankyrin repeat domains 2
13	235004_at	RBM24	RNA binding motif protein 24
14	208451_s_at	C4A /// C4B /// LOC10 complement component 4A (Rodgers blood group) /// compleme	
15	212328_at	LIMCH1	LIM and calponin homology domains 1
16	231472_at	FBXO15	F-box protein 15
17	238983_at	NSUN7	NOP2/Sun domain family, member 7
18	240275_at	ARMC3	armadillo repeat containing 3
19	1552439_s_at	MEGF11	multiple EGF-like-domains 11
20	215193_x_at	HLA-DRB1 /// HLA-DRI	major histocompatibility complex, class II, DR beta 1 /// major hist
21	223838_at	TSGA10	testis specific, 10
22	231077_at	C1orf192	chromosome 1 open reading frame 192
23	208792_s_at	CLU	clusterin
24	204052_s_at	SFRP4	secreted frizzled-related protein 4
25	204719_at	ABCA8	ATP-binding cassette, sub-family A (ABC1), member 8
26	212588_at	PTPRC	protein tyrosine phosphatase, receptor type, C
27	203397_s_at	GALNT3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalacto
28	229095_s_at	LIMS3 /// LIMS3-LOC4	LIM and senescent cell antigen-like domains 3 /// LIMS3-LOC4408
29	211991_s_at	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1
30	233516_s_at	SPAG17	sperm associated antigen 17
31	227188_at	FAM176C	family with sequence similarity 176, member C
32	228554_at	PGR	progesterone receptor
33	215695_s_at	GYG2	glycogenin 2
34	228771_at	ADRBK2	adrenergic, beta, receptor kinase 2
35	1562371_s_at	VWA3B	von Willebrand factor A domain containing 3B
36	222890_at	CCDC113	coiled-coil domain containing 113
37	205027_s_at	MAP3K8	mitogen-activated protein kinase kinase kinase 8
38	202436_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1
39	227662_at	SYNPO2	synaptopodin 2
40	229331_at	SPATA18	spermatogenesis associated 18
41	229012_at	C9orf24	chromosome 9 open reading frame 24
42	229816_at	WDR78	WD repeat domain 78
43	203854_at	CFI	complement factor I
44	219313_at	GRAMD1C	GRAM domain containing 1C
45	210168_at	C6	complement component 6
46	229169_at	TTC18	tetratricopeptide repeat domain 18
47	205413_at	MPPED2	metallophosphoesterase domain containing 2

1	240304_s_at	TMC5	transmembrane channel-like 5
2	223924_at	TTC25	tetratricopeptide repeat domain 25
3	209829_at	FAM65B	family with sequence similarity 65, member B
4	210445_at	FABP6	fatty acid binding protein 6, ileal
5	220614_s_at	ADGB	androglobin
6	202768_at	FOSB	FBJ murine osteosarcoma viral oncogene homolog B
7	202672_s_at	ATF3	activating transcription factor 3
8	227099_s_at	C11orf96	chromosome 11 open reading frame 96
9	214428_x_at	C4A /// C4B /// LOC10 complement component 4A (Rodgers blood group) /// compleme	
10	1552326_a_at	CCDC11	coiled-coil domain containing 11
11	239150_at	SNTN	sentan, cilia apical structure protein
12	236222_at	C3orf15 /// LOC10065 chromosome 3 open reading frame 15 /// uncharacterized LOC10	
13	220269_at	ZBBX	zinc finger, B-box domain containing
14	226863_at	FAM110C	family with sequence similarity 110, member C
15	220110_s_at	NXF3	nuclear RNA export factor 3
16	218901_at	PLSCR4	phospholipid scramblase 4
17	213792_s_at	INSR	insulin receptor
18	243610_at	C9orf135	chromosome 9 open reading frame 135
19	1556158_at	FAM154B	family with sequence similarity 154, member B
20	223315_at	NTN4	netrin 4
21	228692_at	PREX2	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange
22	228241_at	AGR3	factor 2 anterior gradient 3 homolog (Xenopus laevis)
23	201163_s_at	IGFBP7	insulin-like growth factor binding protein 7
24	220390_at	AGBL2	ATP/GTP binding protein-like 2
25	229542_at	C20orf85	chromosome 20 open reading frame 85
26	238116_at	DYNLRB2	dynein, light chain, roadblock-type 2
27	233157_x_at	CCDC114	coiled-coil domain containing 114
28	232745_x_at	SPEF2	sperm flagellar 2
29	217767_at	C3	complement component 3
30	226344_at	ZMAT1	zinc finger, matrin-type 1
31	229831_at	CNTN3	contactin 3 (plasmacytoma associated)
32	210383_at	SCN1A	sodium channel, voltage-gated, type I, alpha subunit
33	236085_at	CAPSL	calcyphosine-like
34	227450_at	ERP27	endoplasmic reticulum protein 27
35	239916_at	WDR16	WD repeat domain 16
36	243802_at	DNAH12	dynein, axonemal, heavy chain 12
37	202948_at	IL1R1	interleukin 1 receptor, type I
38	238625_at	C1orf168	chromosome 1 open reading frame 168
39	240065_at	FAM81B	family with sequence similarity 81, member B
40	231084_at	WDR96	WD repeat domain 96
41	210262_at	CRISP2	cysteine-rich secretory protein 2
42	229170_s_at	TTC18	tetratricopeptide repeat domain 18
43	208498_s_at	ACTG1P4 /// AMY1A / actin, gamma 1 pseudogene 4 /// amylase, alpha 1A (salivary) ///	
44	230093_at	RSPH1	radial spoke head 1 homolog (Chlamydomonas)
45	214945_at	FAM153A /// FAM153 family with sequence similarity 153, member A /// family with sec	
46	200795_at	SPARCL1	SPARC-like 1 (hevin)
47	211990_at	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1

1	223044_at	SLC40A1	solute carrier family 40 (iron-regulated transporter), member 1
3	207802_at	CRISP3	cysteine-rich secretory protein 3

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2 genes)

RefSeq Transcript ID	p-value	Xenografted tumor vs. Normal oviduct		Serous cancer vs
		Fold-Change	p-value	
NM_004004	5.87E-07	194.15	0.0446097	
NM_002026 /// NM_05403	1.82E-07	150.943	0.0001132	
NM_000077 /// NM_00119	2.20E-09	146.365	2.63E-06	
NM_001256099 /// NM_13	1.41E-06	136.964	1.65E-05	
NM_002026 /// NM_05403	2.58E-07	129.223	0.000228229	
NM_002026 /// NM_05403	1.11E-07	122.519	0.000212078	
NM_005978	1.97E-06	111.322	0.000336779	
NM_002026 /// NM_05403	5.67E-08	102.878	0.000180865	
NM_001206846 /// NM_01	4.07E-10	86.748	1.19E-07	
NM_002961 /// NM_01955	5.57E-07	86.1008	0.000314175	
NM_001185056 /// NM_00	7.77E-08	84.8932	0.000783687	
NM_018685	4.17E-07	82.5849	2.17E-06	
NM_004181	4.39E-07	79.0854	0.0176215	
NM_001015886 /// NM_00	3.20E-08	76.9694	0.00244253	
NM_001034 /// NM_00116	8.27E-08	73.2436	9.71E-06	
NM_018492	7.62E-07	71.9627	4.81E-05	
NM_001444	6.05E-11	70.4237	1.20E-07	
NM_002160	7.24E-06	67.1956	0.0413871	
NM_022346	1.06E-09	63.5059	6.73E-08	
NM_001146015 /// NM_01	5.23E-09	62.5462	4.50E-08	
NM_001827	1.07E-08	59.8806	3.97E-06	
NM_021107 /// NM_03336	1.42E-10	58.6994	7.24E-05	
NM_016448	6.18E-11	55.1857	1.36E-08	
NM_001114120 /// NM_01	3.66E-08	54.8264	2.75E-05	
NM_001256799 /// NM_00	8.01E-09	54.8252	0.00313461	
NM_001166691 /// NM_00	2.20E-12	53.1695	2.02E-11	
NM_022346	4.94E-10	53.1519	2.04E-05	
NM_001034 /// NM_00116	3.02E-05	52.5865	0.00140245	
NM_001067	7.37E-09	52.3716	9.75E-10	
NM_001130829 /// NM_00	3.71E-09	51.1075	8.02E-06	
NM_004936 /// NM_07848	7.46E-10	50.3667	0.00496907	
NM_001207042 /// NM_00	8.29E-16	47.9748	5.91E-06	
NM_001067	2.56E-08	47.6484	1.61E-07	
NM_001029989 /// NM_01	4.21E-07	46.8959	9.42E-06	
NM_001002269 /// NM_01	3.63E-09	45.9372	0.0134098	
NM_001130851 /// NM_00	9.15E-11	45.0968	8.25E-07	
NM_018304	6.11E-09	44.7991	2.18E-06	
NM_004219	7.83E-12	44.0016	7.45E-08	
NM_006818	2.38E-12	43.8789	0.000328096	
NM_001255	2.84E-06	43.7721	6.30E-06	
NM_024745	7.16E-13	42.6672	5.67E-07	
NM_001012270 /// NM_00	3.35E-08	42.0438	2.00E-05	
NM_031966	7.24E-08	41.3069	4.42E-06	

1	NM_001114120 /// NM_01	6.40E-09	40.6658	4.96E-05
2	NM_001001790 /// NM_00	4.47E-09	40.4379	0.000971516
3	NM_001127182 /// NM_01	9.34E-08	40.3811	1.95E-07
4	NM_001267580 /// NM_00	1.99E-08	40.1021	1.97E-08
5	NM_004336	3.89E-09	39.5809	8.46E-08
6	NM_000077 /// NM_00119	1.83E-11	39.4114	1.06E-05
7	NM_031423 /// NM_14569	2.02E-11	39.2024	4.90E-12
8	NM_031942 /// NM_14581	3.29E-06	38.0567	0.000915955
9	NM_016448	3.02E-12	37.4461	2.27E-07
10	NM_001198557 /// NM_00	9.62E-09	37.416	2.96E-05
11	NM_005914 /// NM_18274	2.02E-12	37.0746	2.03E-06
12	NM_001129897 /// NM_00	2.86E-08	36.6682	9.65E-09
13	NM_013363	1.18E-08	36.1554	0.00474735
14	NM_001142556 /// NM_00	3.19E-07	35.3182	9.70E-06
15	NM_001813	5.33E-14	34.727	1.20E-06
16	NM_001160706 /// NM_00	6.52E-07	34.0245	0.00658233
17	NM_014176	1.09E-11	33.933	8.95E-05
18	NM_005733	6.54E-10	33.0866	1.87E-10
19	NM_002305	2.75E-10	32.4713	0.0008352
20	NM_002291	2.63E-06	32.3716	0.0311721
21	NM_007019 /// NM_18179	1.29E-10	32.3393	5.21E-10
22	NM_024629	3.85E-10	32.1917	6.61E-08
23	NM_001166356 /// NM_00	1.40E-08	32.095	0.00011338
24	NM_001130829 /// NM_00	1.60E-08	32.0495	3.35E-05
25	NM_001142556 /// NM_00	1.16E-07	32.0253	0.0032725
26	NM_018518 /// NM_18275	3.75E-07	31.5499	0.0160453
27	NM_007274 /// NM_18186	1.37E-10	31.3961	5.81E-05
28	NM_016343	7.88E-10	31.0042	6.16E-09
29	NM_003600 /// NM_19843	5.10E-10	30.9649	5.60E-12
30	NM_174942	1.14E-08	30.7088	1.24E-08
31	NM_012474 /// NR_03743	1.64E-10	30.3586	3.09E-05
32	NM_003878	1.69E-06	30.2673	1.37E-06
33	NM_032756	2.97E-10	30.2069	0.000433131
34	NM_001005413 /// NM_00	6.99E-07	30.1462	2.97E-07
35	NM_007280	7.48E-11	29.4258	0.000273079
36	NM_001114120 /// NM_01	2.03E-09	29.2812	0.00113718
37	NM_001199261 /// NM_00	2.50E-12	28.7377	0.000110883
38	NM_001048201 /// NM_01	3.96E-07	28.549	0.00232417
39	NM_001100910 /// NM_00	4.01E-07	28.5277	5.61E-05
40	NM_001114121 /// NM_00	1.37E-08	28.0585	5.47E-05
41	NM_003600 /// NM_19843	5.43E-11	28.0358	2.02E-10
42	NM_001130829 /// NM_00	8.16E-06	27.4298	2.37E-05
43	NM_030919	7.86E-06	27.3062	1.31E-06
44	NM_001031628 /// NM_00	2.76E-09	27.2913	0.000736861
45	NM_173567	4.29E-09	27.0949	0.000395683
46	NM_001160033 /// NM_00	7.74E-10	26.9468	5.10E-05
47	NM_004298 /// NM_15348	7.69E-08	26.9426	0.000149792

1				
2	NM_000269 /// NM_19817	3.63E-09	26.9322	0.000135352
3	NM_001113378 /// NM_01	6.21E-11	26.6319	4.80E-09
4	NM_014875	2.47E-08	25.8864	1.88E-08
5	NM_001070	7.31E-10	25.7397	2.19E-05
6	NM_001145208 /// NM_01	1.69E-09	25.2949	6.04E-05
7	NM_014096 /// NM_01761	8.44E-10	25.2498	1.46E-05
8	NM_001166496 /// NM_00	8.86E-07	25.105	0.00371699
9	NM_001002799 /// NM_00	6.76E-07	24.856	4.87E-05
10	NM_001168551 /// NM_01	1.01E-13	24.8376	1.34E-08
11	NM_017915	2.45E-11	24.7816	5.54E-05
12	NM_016095	2.53E-10	24.7519	9.86E-07
13	NM_000597	2.69E-05	24.5338	0.000196035
14	NM_001042426 /// NM_00	2.44E-06	24.3145	3.35E-06
15	NM_002703	9.13E-08	24.1661	0.016957
16	NM_012394	2.89E-11	24.1376	1.71E-05
17	NM_001126103 /// NM_00	7.42E-08	23.9965	2.53E-07
18	NM_004701	2.06E-08	23.9216	2.23E-08
19	NM_004702 /// NM_05773	3.81E-09	23.6354	9.74E-05
20	NM_001211	1.79E-06	23.536	4.08E-07
21	NM_001015051 /// NM_00	5.99E-05	23.5275	0.0275818
22	NM_004523	1.37E-07	23.4655	1.38E-07
23	NM_016401 /// NR_024596	2.69E-08	23.4505	0.00973226
24	NM_020675	8.28E-08	23.1727	0.00090201
25	NM_001002032 /// NM_00	3.93E-12	23.0821	1.32E-05
26	NM_006993	8.56E-13	22.6309	3.16E-05
27	NM_001130862 /// NM_00	3.27E-07	22.4118	2.47E-07
28	NM_032043	1.75E-10	22.2716	1.48E-07
29	NM_012112	1.01E-08	22.0444	4.57E-08
30	NM_001166496 /// NM_00	8.99E-06	21.9351	0.0150149
31	NM_001160706 /// NM_00	1.62E-06	21.8339	0.0190539
32	NM_000393	2.96E-06	21.0731	0.00302529
33	NM_020242	2.49E-07	20.9965	2.29E-07
34	NM_004856 /// NM_13855	1.31E-06	20.7476	4.18E-07
35	NM_005914 /// NM_18274	1.05E-09	20.6468	1.07E-06
36	NM_001100624 /// NM_00	5.47E-11	20.4814	2.73E-05
37	NM_001850 /// NM_02035	0.000880386	20.4601	6.14E-05
38	NM_144508 /// NM_17058	3.88E-08	20.1857	0.000110029
39	NM_001256685 /// NM_00	9.76E-06	20.0948	1.34E-06
40	NM_001099286 /// NM_13	1.34E-10	20.0666	6.90E-08
41	NR_024031	6.39E-09	20.059	0.00119736
42	NM_001078166 /// NM_00	8.54E-08	19.9533	0.00791754
43	NM_002623	5.11E-12	19.8218	6.53E-07
44	NM_001098801 /// NM_15	7.14E-08	19.7903	0.00104351
45	NM_001098525 /// NM_01	1.29E-05	19.5518	0.0112875
46	NM_052871 /// NR_015396	2.08E-09	19.5471	0.000430063
47	NM_018004	5.17E-06	19.3835	0.000980456
48	NM_001237	4.02E-07	19.3134	0.00679371

1	NM_001789 /// NM_20156	1.09E-11	19.2628	3.18E-05
2	NM_002592 /// NM_18264	4.53E-07	18.8156	0.000115791
3	NM_005737	6.60E-07	18.7673	9.58E-05
4	NM_018518 /// NM_18275	3.46E-07	18.7542	1.77E-05
5	NM_001009936 /// NM_01	3.10E-08	18.653	7.99E-05
6	NM_001098616 /// NM_01	2.79E-09	18.6266	0.0016783
7	NM_005022	5.24E-07	18.4364	0.0110857
8	NM_152562	2.38E-09	18.3738	1.65E-05
9	NM_001190799 /// NM_00	5.06E-08	18.2961	0.000671851
10	NM_018410	2.13E-09	18.1974	1.72E-08
11	NM_001001563	2.11E-10	18.0096	3.16E-06
12	NM_016037	4.08E-13	17.9771	6.73E-06
13	NM_001193424 /// NM_00	8.83E-09	17.9541	0.000703176
14	NM_080748	1.06E-10	17.7752	1.45E-05
15	NM_001190991 /// NM_01	7.34E-10	17.6389	1.83E-07
16	NM_005105	9.79E-08	17.6105	0.000230946
17	NM_001137604 /// NM_01	6.23E-08	17.3881	0.000295671
18	NM_001009936 /// NM_01	8.28E-08	17.3775	0.00128462
19	NM_001845	6.97E-08	17.3746	0.000269278
20	NM_014317	1.31E-09	17.1415	1.23E-05
21	NM_001130158 /// NM_00	9.23E-08	17.1188	0.000107932
22	NM_018128	2.90E-10	17.1172	0.000402458
23	NM_001002258 /// NM_00	3.20E-06	17.0082	0.00480524
24	NM_031299	7.19E-10	16.983	2.36E-10
25	NM_000075 /// NM_05298	2.16E-07	16.9684	0.000317706
26	NM_000365 /// NM_00115	9.12E-07	16.8595	0.000575207
27	NM_000170	1.17E-05	16.8509	1.20E-05
28	NM_014875	1.96E-11	16.8499	1.83E-07
29	NM_014624	5.41E-08	16.8	0.00135819
30	NM_015341	3.64E-09	16.7458	1.06E-05
31	NM_002318	2.15E-08	16.7454	0.000458976
32	NM_001012507	4.81E-08	16.6607	0.000166421
33	NM_153695	3.45E-06	16.4385	0.00105107
34	NM_014109	3.24E-06	16.4375	4.00E-07
35	NM_001018067 /// NM_00	1.21E-08	16.4358	0.000556296
36	NM_020200	3.18E-05	16.4146	0.0238651
37	NM_006397	3.67E-08	16.3791	1.50E-05
38	NM_014109	6.72E-08	16.2747	0.000150378
39	NM_001905	1.22E-06	16.2653	0.000494056
40	NM_001129897 /// NM_00	1.36E-08	16.2319	9.28E-08
41	NM_001040152 /// NM_00	4.71E-06	16.0033	0.000524252
42	NM_013237	8.13E-11	15.9216	6.79E-06
43	NM_006713	9.97E-12	15.8889	1.36E-05
44	XR_040503	2.12E-06	15.8533	0.00269906
45	NM_001079524 /// NM_00	8.87E-05	15.7932	0.0454423
46	NM_031966	4.68E-08	15.7874	1.83E-07
47	NM_018063	7.39E-10	15.6299	7.06E-06

1				
2	NM_001145966 /// NM_00	1.64E-06	15.6074	0.000354249
3	NM_017785	2.19E-09	15.5705	9.00E-06
4	NM_005916 /// NM_18277	1.45E-06	15.552	7.44E-05
5	NM_001197330 /// NM_00	1.16E-12	15.5076	1.56E-07
6	NM_004559	1.20E-07	15.4581	0.000587199
7	NM_021067	3.76E-10	15.2466	3.13E-11
8	NM_024996	5.33E-07	15.2306	0.00110486
9	NM_006461	5.65E-10	15.1867	3.72E-07
10	NM_001142761 /// NM_00	2.22E-10	15.1837	2.66E-05
11	NM_001270411 /// NM_00	1.97E-05	15.1138	0.0183959
12	NM_005915	1.02E-07	15.095	1.02E-06
13	NM_005034	1.22E-07	15.0357	0.000152316
14	NM_001012270 /// NM_00	1.15E-10	14.8851	6.12E-06
15	NM_178014	2.15E-06	14.8738	0.000549977
16	NM_003142	4.83E-07	14.8137	0.00818877
17	NM_018407	2.49E-05	14.7292	0.000931545
18	NM_001190799 /// NM_00	1.29E-07	14.6136	0.000138719
19	NM_006845	1.38E-07	14.4754	3.21E-09
20	NM_014367	9.32E-09	14.2675	2.14E-06
21	NM_001071	0.000297954	14.1616	0.0022331
22	NM_004044	1.36E-08	14.1593	0.00112029
23	NM_005737	3.97E-07	14.1323	2.96E-05
24	NM_002131 /// NM_14589	7.37E-09	14.1193	0.000307272
25	NM_006234	4.29E-12	14.0097	4.55E-06
26	NM_001178010 /// NM_00	4.14E-08	13.9065	0.00132257
27	NM_001142463 /// NM_00	7.73E-08	13.9015	0.000569094
28	NM_001134693	1.68E-09	13.8741	0.00036413
29	NM_001199779 /// NM_00	1.00E-07	13.8076	1.17E-05
30	NM_003074	3.08E-09	13.7237	0.000515849
31	NM_001025252 /// NM_00	1.15E-07	13.6939	0.00095701
32	NM_080668	3.72E-08	13.6521	1.19E-06
33	NM_178014	1.22E-06	13.5373	0.000454097
34	NM_001145713 /// NM_00	4.16E-08	13.4628	0.000552009
35	NM_052850	2.11E-06	13.4536	0.0150484
36	NM_000532 /// NM_00117	2.03E-06	13.3138	4.07E-05
37	NM_002949	1.30E-08	13.2763	3.17E-05
38	NM_014367	1.76E-09	13.1732	7.67E-07
39	NM_024770	1.11E-06	13.1079	0.00413249
40	NM_001136478 /// NM_00	3.78E-07	13.0845	0.00360709
41	NM_031280	4.87E-08	13.0801	5.72E-06
42	NM_018944	1.45E-06	13.0689	0.000586995
43	NM_002524	1.26E-06	12.8581	0.000255187
44	NM_004559	5.71E-06	12.8256	0.000382104
45	NM_001134419 /// NM_00	9.28E-05	12.7286	0.000277555
46	NM_015201	7.09E-06	12.6794	7.99E-06
47	NM_000365 /// NM_00115	3.23E-07	12.5824	0.000775943
48	NM_023077	2.56E-10	12.4935	8.04E-05
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1	NM_006023	1.33E-06	12.4622	0.00497142
2	NM_033550	9.45E-07	12.4162	0.00570171
3	NM_001270472 /// NM_00	4.41E-07	12.3988	0.00158603
4	NM_006845	1.92E-08	12.3006	9.41E-05
5	NM_001042424 /// NM_00	2.65E-09	12.2896	3.96E-07
6	NM_001258315 /// NM_00	0.000167362	12.2313	6.57E-05
7	NM_001159587 /// NM_00	0.00017269	12.2247	0.0167102
8	NM_003118 /// XR_110317	0.000203278	12.1374	0.000365182
9	NM_003920	4.12E-06	12.1269	8.45E-06
10	NM_001008396 /// NM_00	1.67E-10	12.1163	6.48E-07
11	NM_001199199 /// NM_00	7.96E-05	12.0647	0.0177409
12	NM_005063	0.000563744	12.0537	0.000107354
13	NM_002425	9.39E-06	12.0139	0.00758261
14	NM_001203247 /// NM_00	5.43E-07	11.9823	1.80E-09
15	NM_024094	2.18E-06	11.9311	4.07E-05
16	NR_003604 /// NR_003605	1.31E-08	11.8516	0.000314589
17	NM_002916 /// NM_18157	1.27E-07	11.8242	2.54E-06
18	NM_022366	3.63E-06	11.7808	0.0155641
19	NM_014175	1.62E-06	11.7314	0.00126517
20	NM_014408	9.65E-07	11.7113	0.000867849
21	NM_001256135 /// NM_00	1.65E-06	11.7008	0.000158905
22	NM_002915 /// NM_18155	6.76E-07	11.6909	0.000263607
23	NM_005956	2.41E-07	11.641	0.00108318
24	NM_018256	7.24E-09	11.6251	2.56E-06
25	NM_053040 /// NR_002976	8.50E-08	11.6224	0.00236033
26	NM_022061	2.60E-08	11.5667	0.00147004
27	NM_003875	1.38E-10	11.4972	7.80E-07
28	NM_133259	2.47E-08	11.3777	0.00108183
29	NM_152308	1.51E-12	11.3364	2.18E-08
30	NM_002105	1.12E-07	11.2902	0.0010435
31	NM_001130929 /// XM_00	2.30E-09	11.2823	1.04E-05
32	NM_013296	5.21E-05	11.2818	3.89E-05
33	NM_024006 /// NM_20682	5.54E-07	11.267	0.0030102
34	NM_001134231 /// NM_02	5.27E-09	11.2389	0.000443954
35	NM_001144757 /// NM_00	0.00100541	11.2111	0.00204246
36	NM_001025252 /// NM_00	0.00013749	11.1891	0.00985254
37	NM_012310	4.60E-06	11.1871	0.00255567
38	NM_014184	3.35E-06	11.1588	0.0101764
39	NM_001042422 /// NM_00	1.63E-05	11.087	0.0021603
40	NM_006938	1.64E-09	11.0352	0.000221657
41	NM_001105573	7.20E-06	11.0227	0.000616816
42	NM_001114121 /// NM_00	1.32E-09	10.9517	4.31E-05
43	NM_001011667 /// NM_00	1.73E-08	10.9288	2.72E-07
44	NM_178014	1.78E-05	10.9233	0.00886206
45	NM_001100624 /// NM_00	6.40E-13	10.8984	7.32E-09
46	NM_012293	7.96E-07	10.8981	0.000182296
47	NM_007051 /// NM_13191	8.42E-08	10.8434	0.000304594

1				
2	NM_001243088 /// NM_00	2.40E-07	10.7614	6.21E-07
3	NM_001040649 /// NM_00	9.07E-08	10.7344	0.000572196
4	NM_021154 /// NM_05817	0.000254735	10.7297	0.000131146
5	NM_001660	4.70E-05	10.7063	0.00280085
6	NM_001826 /// NR_024163	1.32E-05	10.6633	0.000441453
7	NM_001164623 /// NM_01	7.34E-07	10.5899	0.00420544
8	NM_0018063	3.11E-07	10.5898	0.000117132
9	NM_005952	2.42E-05	10.5687	0.0159862
10	NM_001167924 /// NM_03	7.54E-09	10.5548	0.000392885
11	NM_001206846 /// NM_01	2.27E-06	10.5212	5.67E-07
12	NM_020890	8.46E-08	10.4803	0.00138424
13	NM_001160033 /// NM_00	5.81E-08	10.4519	1.86E-06
14	NM_001080443 /// NM_00	1.10E-09	10.3847	1.92E-10
15	NM_004483 /// NR_033249	3.42E-06	10.3334	0.0113283
16	NM_173529	3.41E-05	10.2641	0.00716291
17	NM_001024934 /// NM_00	6.25E-06	10.264	0.00762005
18	NM_032485 /// NM_18280	7.89E-08	10.2456	3.27E-07
19	NM_024098	4.66E-10	10.1812	8.28E-05
20	NM_006638	1.34E-06	10.1638	0.00109895
21	NM_018270	6.76E-09	10.1564	3.17E-06
22	NM_001164269 /// NM_00	4.20E-08	10.1246	2.82E-05
23	NM_005914 /// NM_18274	1.01E-10	10.0515	6.40E-06
24	NM_001026 /// NM_00114	9.98E-05	10.0478	0.00511145
25	NM_001002258 /// NM_00	5.20E-05	10.0361	0.00130069
26	NM_019037	1.19E-06	9.97758	0.000644199
27	NM_001165031 /// NM_01	3.69E-08	9.944	0.000920281
28	NM_020726	1.80E-07	9.89334	0.00028814
29	NM_001256510 /// NM_00	2.81E-05	9.88044	0.0177325
30	NM_024629	3.14E-05	9.77945	0.000903816
31	NM_007033	7.05E-07	9.76743	0.00400491
32	NM_001256875 /// NM_01	1.44E-07	9.72026	5.91E-07
33	NM_001204182 /// NM_00	1.50E-05	9.69364	0.000669006
34	NM_001165031 /// NM_01	1.33E-07	9.67846	0.000107569
35	NM_030928	1.31E-09	9.67761	6.13E-05
36	NR_040001	0.000351759	9.62634	0.0307327
37	NM_000310 /// NM_00114	1.35E-05	9.58299	0.00594439
38	NM_004052	1.94E-05	9.57858	0.000262759
39	NM_001258437 /// NM_00	2.28E-07	9.549	0.00116143
40	NM_001128210 /// NM_18	5.02E-07	9.53261	0.00192102
41	NM_001042762 /// NM_02	0.000115937	9.51958	0.00954669
42	NM_001789 /// NM_20156	4.62E-08	9.50461	8.79E-06
43	NM_001201483 /// NM_00	2.81E-05	9.46185	0.00372617
44	NM_002770	2.17E-06	9.39128	0.00123976
45	NM_015261	2.81E-06	9.38803	0.00212995
46	NM_002266	5.93E-05	9.37303	0.00253773
47	NM_002770	3.25E-07	9.35325	0.00232863
48	NM_002634	1.56E-05	9.3495	0.0059617

1	NM_014171	1.47E-06	9.32183	0.000433403
2	NM_024037	1.22E-09	9.31114	1.25E-08
3	NM_016035	4.73E-07	9.2694	0.000566425
4	NM_020409 /// NM_17798	5.03E-10	9.24512	1.54E-05
5	NM_024808	9.40E-05	9.22064	0.00248125
6	NM_006848	7.36E-06	9.21135	0.00219912
7	NM_023937	1.62E-06	9.2026	0.000107653
8	NM_014467	7.17E-06	9.20018	0.000399589
9	NM_000034 /// NM_00112	7.70E-05	9.18701	0.00699727
10	NM_020750	2.23E-10	9.17217	1.34E-05
11	NM_004301 /// NM_17798	7.08E-06	9.09358	0.000389137
12	NM_001790 /// NM_02280	2.22E-07	9.09056	8.97E-07
13	NM_001128211 /// NM_03	0.000131978	9.01149	0.000773952
14	NM_001113378 /// NM_01	3.34E-08	9.00985	1.35E-06
15	NM_001256799 /// NM_00	1.02E-05	8.97219	0.0014149
16	NM_032390	4.34E-08	8.95564	0.0002534
17	NM_001243120 /// NM_00	6.47E-05	8.95344	0.00283373
18	NM_138689	8.39E-06	8.94943	0.000496815
19	NM_006101	6.12E-05	8.92635	8.00E-07
20	NM_000088	2.26E-06	8.85924	0.000476974
21	NM_006802	8.37E-06	8.82491	0.00489482
22	NM_198066	7.52E-05	8.76015	0.0136224
23	NM_000071 /// NM_00117	0.000147148	8.71307	0.00222914
24	NM_001198812 /// NM_00	0.000206951	8.6928	6.60E-05
25	NM_001172303 /// NM_00	3.05E-06	8.68226	0.000455216
26	NM_000057	9.78E-08	8.62648	6.11E-07
27	NM_001166356 /// NM_00	1.93E-08	8.62202	2.23E-07
28	NM_002074	1.65E-06	8.5927	0.000583086
29	NM_001002799 /// NM_00	0.000298024	8.57285	0.00463527
30	NM_001199534 /// NM_00	6.24E-06	8.555	0.000130516
31	NM_001080449	1.15E-07	8.55234	2.96E-06
32	NM_024899	1.54E-07	8.54779	0.0010084
33	NM_001845	3.80E-06	8.54282	0.00113215
34	NM_004373	4.36E-05	8.52075	0.00972443
35	NM_001135570 /// NR_024	1.96E-05	8.4784	0.00198926
36	NM_138462	2.29E-06	8.47374	0.00147492
37	NM_004526	8.53E-06	8.4658	2.18E-05
38	NM_019042	4.77E-07	8.4411	0.000125268
39	NM_006558	8.51E-05	8.4241	0.00655065
40	NM_001143936	4.75E-05	8.36492	0.00347382
41	NM_002577	2.05E-06	8.36449	0.000121671
42	NM_013237	6.65E-06	8.3348	0.00303712
43	NM_032479	2.94E-08	8.32468	0.000156817
44	NM_023080	0.000396559	8.30749	0.00271216
45	NM_004146	7.75E-06	8.2795	0.00141556
46	NM_004395 /// NM_08088	1.17E-06	8.26667	4.92E-07
47	NM_013299	1.31E-05	8.23892	2.29E-06

1				
2	NM_000425 /// NM_00114	0.000999044	8.22723	2.98E-06
3	NM_001001790 /// NM_00	1.92E-05	8.21173	0.0101217
4	NM_001135247 /// NM_00	0.000278273	8.20701	7.93E-06
5	NM_014171	5.88E-06	8.18042	0.00073109
6	XR_109352 /// XR_109353	9.78E-07	8.17968	0.00285912
7	NM_005805	3.09E-05	8.17548	0.0171708
8	NM_003088 /// XR_132832	1.61E-06	8.17253	3.45E-05
9	NM_001166017 /// NM_14	2.13E-08	8.07039	1.66E-05
10	NM_001042517 /// NM_00	1.93E-05	8.06941	0.0020882
11	NM_001105237 /// NM_01	1.69E-07	8.05712	0.00030664
12	NM_017915	1.65E-08	8.01621	6.43E-07
13	NM_001206846 /// NM_01	2.16E-07	7.994	1.21E-07
14	NM_001077516 /// NM_00	1.02E-07	7.93906	0.000241526
15	NM_014865	0.000353321	7.92715	0.00263073
16	NM_001039954	3.93E-05	7.92352	0.011369
17	NM_004341	1.84E-08	7.87212	3.94E-06
18	NM_022459	2.02E-09	7.82015	1.36E-05
19	NM_030782	0.000133018	7.80414	0.00200008
20	NM_005063	0.000574103	7.77791	0.000179549
21	NM_001164391 /// NM_00	1.72E-06	7.77559	4.92E-05
22	NM_001256725 /// NM_00	4.62E-08	7.76835	0.000269761
23	NM_001145725 /// NM_01	3.65E-06	7.76108	0.00234654
24	NM_001015885 /// NM_00	4.21E-07	7.72119	1.81E-05
25	NR_038253 /// NR_038254	4.06E-08	7.69968	7.03E-08
26	NM_033109	4.23E-06	7.69736	0.000326574
27	NM_001256799 /// NM_00	1.51E-05	7.55735	0.00179303
28	NM_001517	2.72E-05	7.54978	0.000790678
29	NM_001253900 /// NM_00	0.000322274	7.54569	2.91E-06
30	NM_001166131 /// NM_15	9.92E-08	7.53626	7.36E-09
31	NM_015190	2.04E-05	7.51883	0.000304021
32	NM_001166260 /// NM_00	0.000229685	7.50922	0.033416
33	NM_001143964 /// NM_00	2.38E-05	7.47162	2.92E-05
34	NM_031299	1.14E-09	7.46256	1.91E-06
35	NM_001031713 /// NM_02	1.88E-07	7.4542	0.000410814
36	NM_002293	3.05E-06	7.43828	7.75E-05
37	NM_000088	4.72E-05	7.3991	0.0110042
38	NM_015969	5.38E-06	7.38655	0.000944154
39	NM_145018	4.42E-07	7.37207	0.000315027
40	NM_001037334 /// NM_00	4.23E-07	7.36338	0.000583764
41	NM_015938	7.45E-05	7.35618	0.0176771
42	NM_001258392 /// NM_00	1.27E-08	7.34386	1.27E-05
43	NM_033112	5.84E-05	7.30934	0.00584353
44	NM_016072	4.01E-05	7.30295	0.000507433
45	NM_001853	0.0354386	7.23274	0.0176609
46	NM_007051 /// NM_13191	1.39E-07	7.23199	0.000299323
47	NM_198566	1.46E-06	7.22182	1.38E-06
48	NM_032881	8.63E-07	7.21584	0.000892514

1	NM_001152	0.000501444	7.18788	0.0197753
2	NM_001008800 /// NM_00	1.14E-05	7.16841	0.00399018
3	NM_000373 /// NR_033434	4.21E-05	7.14078	0.00284915
4	NM_001048166 /// NM_00	6.40E-06	7.11008	2.08E-05
5	NM_001008396 /// NM_00	2.61E-05	7.10511	0.000499648
6	NM_053040 /// NR_002976	9.64E-05	7.09943	0.0127575
7	NM_000034 /// NM_00112	6.29E-05	7.09628	0.00233028
8	NM_032361 /// NR_003611	7.56E-07	7.08486	0.00013073
9	NM_017955 /// NM_14570	7.97E-08	7.05468	1.16E-05
10	NM_003074	3.33E-05	7.05221	0.00421035
11	NM_003107	0.00148803	7.02416	0.00721192
12	NM_001079669 /// NM_03	0.000100412	7.01266	0.000502035
13	NM_001261834 /// NM_00	1.01E-05	7.01071	0.000271263
14	NM_006342	7.19E-05	7.00201	2.40E-06
15	NM_001199534 /// NM_00	5.99E-05	6.98841	0.000265874
16	NM_005951	0.000211003	6.98674	0.0150353
17	NM_001127181 /// NM_00	6.96E-08	6.94256	7.34E-06
18	NM_001260474 /// NM_00	4.27E-07	6.93479	0.00012781
19	NM_001197292 /// NM_00	2.94E-05	6.89855	0.00112758
20	NM_001205206 /// NM_00	9.93E-07	6.86303	1.66E-05
21	NM_016027	0.00199933	6.84894	0.0306835
22	NM_001256135 /// NM_00	0.000472848	6.81957	0.00039836
23	NM_031420	4.62E-07	6.8019	0.000218683
24	NM_001238 /// NM_05718	0.000150381	6.79781	1.32E-07
25	NM_001724 /// NM_19918	0.000186928	6.79582	0.0217445
26	NM_152416 /// XR_108868	0.000501907	6.77023	0.00641851
27	NM_000289 /// NM_00116	1.30E-07	6.76725	1.18E-05
28	NM_199420	1.94E-05	6.74497	7.39E-08
29	NM_153339	1.41E-09	6.74433	1.38E-05
30	NM_006739	0.00019922	6.73184	0.00668764
31	NM_006190 /// NR_033911	8.31E-07	6.67255	0.000164614
32	NM_001159673 /// NM_00	0.00076998	6.66992	0.00464664
33	NM_019037	4.01E-05	6.66003	0.000618947
34	NM_145287 /// NR_033354	6.05E-07	6.65597	0.000434341
35	NM_001136264 /// NM_00	2.69E-05	6.64854	0.00733811
36	NM_016397 /// NM_19897	2.65E-06	6.63588	0.000426956
37	NM_001195563 /// NM_00	0.000142545	6.63498	0.0019235
38	NM_001256798 /// NM_08	0.000184458	6.63222	7.34E-05
39	NM_012334	0.000581262	6.61682	3.34E-05
40	NM_023009 /// NR_052851	1.02E-05	6.61307	2.95E-06
41	NM_000175 /// NM_00118	4.02E-06	6.61233	1.52E-05
42	NM_023077	3.64E-09	6.58166	4.89E-06
43	NR_024388	1.38E-05	6.56947	3.33E-05
44	NM_001012985 /// NM_00	2.17E-05	6.56895	0.00195446
45	NM_001686	3.29E-05	6.55901	0.00416093
46	NM_003088 /// XR_132832	1.69E-07	6.55675	0.000238847
47	NM_001697	0.00160362	6.53291	0.022597

1				
2	NM_016567 /// NM_07846	4.56E-05	6.52492	0.00152445
3	NM_001184979 /// NM_00	9.65E-08	6.50628	9.47E-06
4	NM_001077484 /// NM_03	7.58E-07	6.4934	8.53E-06
5	NM_005837	6.90E-07	6.4787	0.000928026
6				
7	NM_020647	0.000236816	6.47645	0.000937137
8	NM_012334	2.69E-05	6.45122	1.61E-06
9	NM_006265	9.51E-06	6.44537	0.000288851
10	NM_001044385 /// NM_15	7.24E-07	6.43354	0.000365912
11				
12	NM_005949	0.000213695	6.37279	0.00367584
13	NM_000034 /// NM_00112	8.17E-05	6.37069	0.00251322
14	NM_015459	6.26E-06	6.33627	0.000121874
15				
16	NM_001024210 /// NM_00	3.55E-06	6.30081	0.00142175
17	NM_001042618 /// NM_00	7.95E-07	6.29112	4.86E-05
18	NM_004111	3.04E-06	6.28725	7.00E-06
19	NM_014321 /// NR_037620	1.09E-07	6.28132	4.69E-08
20				
21	NM_000465	5.83E-06	6.25735	7.29E-05
22	NM_001145966 /// NM_00	1.96E-07	6.25572	2.05E-06
23	NM_023008 /// NM_17815	3.68E-05	6.24466	0.00157128
24	NM_199249 /// NM_19925	9.85E-06	6.23958	0.0026748
25				
26	NM_032174	2.37E-07	6.23803	0.000126517
27	NM_199287	2.80E-05	6.23668	0.00194555
28	NM_006500	0.000104543	6.22565	0.00215916
29	NM_016397 /// NM_19897	1.89E-05	6.18913	0.00109841
30				
31	NM_001033521 /// NM_00	1.53E-08	6.18674	1.81E-06
32	NM_001256799 /// NM_00	2.94E-05	6.17178	0.00301906
33	NM_001127229 /// NM_00	2.60E-06	6.14899	0.000315268
34	NM_014426 /// NM_15222	1.03E-07	6.14198	4.02E-05
35				
36	NM_016343	2.15E-05	6.12622	2.01E-09
37	NM_000271	1.96E-05	6.11955	0.000115787
38	NM_016426	1.85E-06	6.11924	7.25E-07
39	NM_018385	1.42E-05	6.10364	0.000414676
40				
41	NM_053042	2.24E-05	6.10015	0.00324768
42	NM_004637	5.73E-05	6.0792	0.00207881
43	NM_024899	0.000205455	6.07861	0.000727947
44	NM_001145454 /// NM_00	8.25E-08	6.0742	2.79E-10
45				
46	NM_016625	1.13E-06	6.06727	1.59E-06
47	NM_016094	2.22E-05	6.06613	4.14E-05
48				
49	NM_001031827 /// NM_00	1.66E-07	6.05419	2.13E-05
50	NM_001256799 /// NM_00	7.52E-06	6.02815	0.00118694
51				
52	NM_001243251 /// NM_02	5.13E-06	5.9996	0.000355568
53	NM_001171155 /// NR_03	1.37E-07	5.99665	1.30E-05
54				
55	NM_031280	6.93E-05	5.99322	8.62E-05
56	NM_013438 /// NM_05306	2.50E-05	5.97406	0.00463059
57				
58	NM_001008709 /// NM_00	2.95E-06	5.97162	0.000511441
59	NM_001033673 /// NM_00	2.88E-05	5.93668	0.00316105
60				
58	NM_001042371	3.74E-05	5.9311	0.000643163
59	NM_001098424 /// NM_00	1.78E-05	5.92098	0.00138084

1	NM_001105573	1.94E-05	5.89083	4.67E-05
2	NM_003091 /// NM_19821	1.10E-06	5.88461	1.03E-07
3	NM_031420	5.57E-06	5.86508	0.000312334
4	NM_013402 /// NR_031729	0.000139097	5.86504	0.00074102
5	NM_024830	5.94E-08	5.8642	1.62E-07
6	NM_001185181 /// NM_00	5.44E-06	5.85736	0.000466613
7	NM_001199981 /// NM_00	7.61E-06	5.85331	0.00227409
8	NM_023071	0.000469537	5.84458	0.00661612
9	NM_001256604 /// NM_00	5.52E-05	5.82965	0.000376833
10	NM_006579	1.42E-05	5.82412	0.000343645
11	NM_014708	2.47E-05	5.82197	6.83E-05
12	NM_032139	0.000760409	5.78694	0.00218295
13	NM_001127325 /// NM_00	2.12E-05	5.75812	0.000319226
14	NM_001102592 /// NM_14	3.14E-05	5.75529	3.19E-06
15	NM_001097612 /// NM_00	1.36E-05	5.75482	0.0026755
16	NM_001130112 /// NM_00	0.000531852	5.74619	0.00802145
17	NM_001256269 /// NM_00	7.97E-07	5.72946	1.05E-06
18	NM_001135673 /// NM_02	0.00086081	5.72457	0.00603027
19	NM_001146160 /// NM_03	0.000723107	5.70399	0.00878637
20	NM_005952	0.000328415	5.69946	0.0162433
21	NM_017850	6.47E-05	5.6586	0.000911804
22	NM_001005290 /// NM_00	3.95E-05	5.65156	6.50E-07
23	NM_014388	2.10E-05	5.64937	0.00391551
24	NM_000858 /// NM_00115	0.00061228	5.64545	0.0203927
25	NM_182513	1.25E-05	5.63859	1.21E-07
26	NM_001130146 /// NM_00	0.000529636	5.63543	0.000248397
27	NM_001199629 /// NM_00	0.000843475	5.60946	0.0014778
28	NR_002578 /// NR_002746	7.02E-05	5.60451	0.000726355
29	NM_012291	1.39E-06	5.60136	4.31E-10
30	NM_004395 /// NM_08088	1.28E-09	5.59309	2.53E-07
31	NM_002792 /// NM_15225	0.000340561	5.58533	0.00275967
32	NM_001201370 /// NM_01	0.000328632	5.5474	0.00423544
33	NM_013402 /// NR_031729	2.65E-06	5.5437	0.000927845
34	NM_000373 /// NR_033434	5.23E-06	5.51858	0.000184773
35	NM_001252129 /// NM_01	0.000476606	5.48928	0.000184469
36	NM_001128626 /// NM_00	0.000157649	5.4872	0.0048277
37	NM_001190991 /// NM_01	0.00122084	5.47546	0.00236218
38	NM_006496	9.93E-05	5.42951	0.00473491
39	NM_001127229 /// NM_00	5.38E-06	5.41598	0.000606432
40	NM_001194998 /// NM_01	0.000100559	5.41331	0.00223947
41	NM_178547	9.70E-06	5.41213	0.00195664
42	NM_003362 /// NM_08091	0.000502259	5.41189	0.000998251
43	NM_004358 /// NM_02187	1.39E-05	5.40257	0.000244301
44	NM_016131	0.00052409	5.40102	0.00525616
45	NM_001185181 /// NM_00	2.15E-05	5.38559	0.00130755
46	NM_001199260 /// NM_02	0.00191061	5.37128	0.0350817
47	NM_001039479 /// NM_01	0.000704058	5.3604	0.00675486

1	NM_001163817 /// NM_00	0.000335869	5.33585	0.00104173
2	NM_001145822 /// NM_00	1.27E-05	5.33326	0.000904834
3	NM_001204057 /// NM_00	1.11E-07	5.31753	9.52E-08
4	NM_031942 /// NM_14581	0.000140473	5.3091	0.00800785
5	NM_001005386 /// NM_00	4.18E-10	5.30506	9.56E-07
6	NM_001256126 /// NM_20	0.000168436	5.30129	0.000714218
7	NM_032242	2.00E-07	5.2971	5.67E-08
8	NM_001142548 /// NM_00	4.25E-05	5.2934	1.34E-07
9	NM_018067	2.74E-05	5.2867	0.00160911
10	NM_002496 /// NR_039840	2.78E-05	5.27343	0.000189932
11	NM_005690 /// NM_01206	0.00267635	5.26332	0.0259922
12	NM_012456	0.000201598	5.2469	0.00170441
13	NM_001042618 /// NM_00	6.70E-08	5.22448	1.46E-05
14	NM_001040649 /// NM_00	6.79E-07	5.22343	1.85E-05
15	NM_017518 /// NM_20710	4.32E-05	5.2036	0.00378857
16	NM_001941 /// NM_02442	0.011172	5.19978	0.0293705
17	NM_003364 /// NM_18159	0.000227056	5.19762	0.00495893
18	NM_001204857 /// NM_00	0.000991926	5.18454	0.00488547
19	NM_001195193 /// NM_00	0.00147273	5.17843	0.0182266
20	NM_001079809 /// NM_13	1.44E-07	5.16837	1.42E-05
21	NM_005005	2.81E-05	5.16582	7.90E-05
22	NM_001025242 /// NM_00	1.61E-05	5.16127	0.000303783
23	NM_001134671 /// NM_02	2.60E-06	5.15771	3.65E-05
24	NM_001136469 /// NM_02	0.00108724	5.15656	0.00306273
25	NM_001042717 /// NM_03	2.58E-06	5.14149	0.000107551
26	NM_000284 /// NM_00117	0.000205223	5.13479	0.000372561
27	NM_014754	8.07E-06	5.13279	5.09E-05
28	NM_018086	0.024518	5.11025	0.0028863
29	NM_001080502 /// NM_17	0.00155633	5.10911	6.64E-07
30	NM_001195602 /// NM_00	4.21E-05	5.0979	0.0025997
31	NM_016397 /// NM_19897	4.68E-06	5.09428	0.00016499
32	NM_001201370 /// NM_01	0.00110299	5.08755	0.0107557
33	NM_021103	8.51E-07	5.07527	6.95E-05
34	NM_001145939 /// NM_00	5.72E-08	5.06936	2.61E-07
35	NM_005189 /// NM_03264	0.000302825	5.06819	8.24E-06
36	NM_001003713 /// NM_00	0.000947057	5.06489	0.00519154
37	NM_001257137 /// NM_00	1.24E-06	5.06193	5.28E-07
38	NM_213720	0.000391168	5.05791	0.000721802
39	NM_001033549 /// NM_01	3.76E-07	5.05617	3.06E-07
40	NM_001142805 /// NM_00	6.68E-05	5.04308	1.44E-05
41	NM_014109	0.000206317	5.01992	4.22E-06
42	NM_001109903 /// NM_03	6.18E-05	5.0035	8.61E-06
43	NM_002792 /// NM_15225	9.93E-05	4.97334	0.00206053
44	NM_001166356 /// NM_00	1.54E-06	4.95916	1.04E-06
45	NM_052969	2.13E-05	4.94927	1.31E-06
46	NM_002263	5.84E-08	4.93289	1.29E-05
47	NM_001320	0.000892431	4.88716	0.00380502

1	NM_001256820 /// NM_00	0.000113106	4.88295	0.00054642
2	NM_001001503 /// NM_02	7.71E-05	4.88047	0.000517602
3	NM_206908 /// NM_20691	0.000346198	4.86471	0.000187654
4	NM_015918 /// NM_19820	0.000390257	4.8601	0.00602586
5	NM_005950	0.000833189	4.85811	0.011175
6	NM_001135653 /// NM_00	2.53E-06	4.8568	1.41E-05
7	NM_032360	8.42E-07	4.8521	0.00011461
8	NM_001142805 /// NM_00	9.88E-05	4.84444	2.50E-05
9	NM_001163812 /// NM_00	8.38E-06	4.84332	5.09E-05
10	NM_018086	0.00175667	4.84128	8.40E-06
11	NM_007027	0.000116507	4.79756	0.000939402
12	NM_001109938 /// NM_00	0.000113216	4.79159	0.00147271
13	NM_001080416 /// NM_00	0.00668883	4.78242	0.00465192
14	NM_001039375 /// NM_02	7.12E-08	4.78017	2.88E-06
15	NM_001863	3.55E-05	4.77496	5.15E-05
16	NM_001099282 /// NM_00	6.88E-06	4.76683	0.000328413
17	NM_001243891 /// NM_00	1.46E-05	4.76119	0.000267633
18	NM_001193513 /// NM_00	4.83E-06	4.74797	0.000300147
19	NM_001419	0.0014129	4.74714	0.010918
20	NM_006602	0.000317217	4.72465	0.00304931
21	NM_001195228 /// NM_01	1.05E-05	4.71578	3.96E-05
22	NM_022552 /// NM_15375	2.18E-05	4.71459	8.02E-07
23	XR_109242 /// XR_111621	0.000768167	4.69198	0.00349431
24	NM_001256119 /// NM_00	4.83E-06	4.68907	0.000103507
25	NM_001267810 /// NM_00	6.51E-05	4.68609	0.000655966
26	NM_016397 /// NM_19897	8.76E-06	4.68536	0.000207472
27	NM_001142474 /// NM_00	4.18E-05	4.67286	7.54E-06
28	NM_001038628 /// NM_00	0.0161805	4.66585	0.0410936
29	NM_001006622 /// NM_00	0.00267397	4.66445	0.00489509
30	NM_001258338 /// NM_01	0.00824853	4.65703	0.0339504
31	NM_001127393 /// NM_00	0.00108965	4.64726	0.00937958
32	NM_006347	7.33E-05	4.61767	0.000600879
33	NM_001130721 /// NM_02	0.000564557	4.6157	0.00157262
34	NM_001105530 /// NM_00	0.000600325	4.602	0.00847569
35	NM_005494 /// NM_05824	0.00106173	4.59975	0.00180718
36	NM_001099670 /// NM_00	9.88E-05	4.59401	0.000548429
37	NM_144772	2.54E-05	4.59303	0.000100701
38	NM_002610	0.00581303	4.58019	0.0021737
39	NM_012456	3.55E-05	4.57541	0.000597544
40	NM_004442 /// NM_01744	0.000957439	4.56973	6.68E-05
41	NM_018407	0.0251241	4.55202	0.0232763
42	NM_001199199 /// NM_00	0.00226781	4.51892	0.00931295
43	NM_018056	2.47E-07	4.51874	2.10E-06
44	NM_152374	0.000100738	4.49951	2.31E-05
45	NM_002264 /// NR_026698	0.000103389	4.49679	0.000988337
46	NM_007276 /// NM_01658	7.49E-05	4.49486	0.000505177
47	NM_001005353 /// NM_01	0.0017267	4.49043	0.00294586

1				
2	NM_001080415	0.000354379	4.48641	0.00138196
3	NM_033416	4.01E-08	4.48041	4.99E-06
4	NM_006231	5.61E-05	4.47592	0.00181557
5	NM_005916 /// NM_18277	9.15E-05	4.47235	2.14E-05
6				
7	NM_012291	1.46E-05	4.47167	5.86E-09
8	NM_032336	1.06E-07	4.45557	8.53E-06
9	NM_203288	0.00176833	4.45219	0.0181816
10	NM_001207014 /// NM_00	0.00585986	4.41797	0.0156035
11				
12	NM_017975 /// NR_003105	0.00317661	4.40978	0.0033077
13	NM_016200	4.25E-06	4.4049	0.00012479
14	NM_001145408 /// NM_00	3.39E-05	4.39734	3.51E-05
15	NM_003404 /// NM_13932	0.00124982	4.39501	0.00852163
16				
17	NM_001202498 /// NM_00	0.000147282	4.36429	0.00122068
18	NM_020782	0.0102134	4.36405	0.0162177
19	NM_001130524 /// NM_03	0.000562233	4.36168	0.00950217
20				
21	NM_002452 /// NM_19894	1.85E-05	4.34971	1.14E-05
22	NM_001105198 /// NM_00	0.00103893	4.34851	0.0102236
23	NM_020158	1.54E-05	4.33987	0.000523834
24	NM_002293	0.000319123	4.32336	0.00611505
25				
26	NM_015965	0.00205367	4.31309	0.0222284
27	NM_001166050 /// NM_00	0.000100017	4.30342	0.00283825
28	NM_001199534 /// NM_00	0.000104392	4.30284	7.89E-05
29	NM_001033505 /// NM_00	3.00E-05	4.30096	1.39E-05
30				
31	NM_001136204 /// NM_01	2.34E-08	4.29256	8.45E-07
32	NM_001134337 /// NM_00	1.09E-05	4.28757	0.000140258
33	NM_004596	0.000360833	4.28481	0.000805824
34	NM_000821 /// NM_00114	0.0018421	4.28171	0.000106338
35				
36	NM_001083946 /// NM_01	7.35E-06	4.2756	0.000215406
37	NM_001242597 /// NM_00	2.74E-05	4.25308	3.74E-05
38	NM_001256604 /// NM_00	0.000593889	4.25261	3.63E-05
39				
40	NM_025049	8.13E-05	4.228	7.04E-05
41	NM_004134	0.000510516	4.22615	0.00644384
42				
43	NM_014367	1.16E-06	4.21649	2.10E-06
44	NM_014344	4.93E-05	4.21249	0.000121087
45				
46	NM_174910	0.00147292	4.20814	0.00202614
47	NM_001080539 /// NM_17	0.000973746	4.20396	2.81E-06
48	NM_003091 /// NM_19821	0.00010551	4.18839	1.07E-05
49				
50	NM_014762	0.000349551	4.18403	0.00331796
51	NM_024857	4.80E-05	4.18331	0.000264878
52				
53	NM_001098786 /// NM_01	0.00437713	4.18323	0.00926028
54	NM_000071 /// NM_00117	0.00291774	4.18081	0.00115307
55				
56	NM_001142805 /// NM_00	0.00012772	4.15564	0.000406182
57	NM_001130963 /// NM_01	0.000544423	4.1472	0.00666539
58				
59	NM_012334	0.00153584	4.12942	0.00267541
60	NM_001198915 /// NM_00	1.81E-05	4.07757	2.07E-05
	NM_000428	6.19E-05	4.07363	0.000335661
	NM_006265	0.00506101	4.07123	0.00832928

1	NM_001034833 /// NM_01	3.49E-05	4.0555	0.00088001
2	NM_001001653 /// NM_05	3.28E-05	4.03528	8.01E-05
3	NM_006733	2.17E-05	4.01095	2.82E-07
4	NM_016407	0.000517893	3.99772	0.00413558
5	NM_001010866 /// NM_00	3.02E-06	3.97999	9.40E-05
6	NM_001130107 /// NM_00	0.000117498	3.97915	0.000589247
7	NM_014109	0.000439593	3.94904	1.97E-05
8	NM_001256135 /// NM_00	0.00850796	3.94753	0.00109158
9	NM_001142805 /// NM_00	6.60E-05	3.94337	2.36E-05
10	NM_017563	0.00778659	3.93357	0.00292281
11	NM_001004339	0.00153929	3.92957	0.00169458
12	NM_001003398 /// NM_00	0.0244205	3.92839	0.00798458
13	NM_022157	0.000393388	3.92635	0.00195498
14	NM_004990	1.29E-05	3.92607	0.000259271
15	NM_080652	8.25E-06	3.8937	2.68E-05
16	NM_007263 /// NM_19944	0.000908682	3.88505	0.00145926
17	NM_032340	7.13E-06	3.87567	2.69E-05
18	NM_005866 /// NM_14715	9.62E-06	3.86621	0.000125989
19	NM_002514	0.0132277	3.85987	0.00118288
20	NM_003765	4.37E-06	3.85792	3.44E-06
21	NM_001105570	0.00221634	3.84693	0.00188982
22	NR_000008 /// NR_002559	1.48E-05	3.83405	3.08E-05
23	NM_001247996 /// NM_01	0.0045165	3.80707	0.00361469
24	NM_001042540 /// NM_00	0.00118579	3.80292	2.50E-06
25	NM_001184740 /// NM_00	0.000376322	3.79496	9.94E-05
26	NM_001142474 /// NM_00	0.00407783	3.78253	0.000969146
27	NM_001039538 /// NM_00	0.000543518	3.78161	0.000122642
28	NM_019070 /// NR_03367	0.000103849	3.77741	0.000648795
29	NM_001166050 /// NM_00	0.00830175	3.77474	0.0331506
30	NM_005737	0.000400399	3.75508	0.000105146
31	NM_001076785 /// NM_00	0.000227049	3.74721	0.00108541
32	NM_001077484 /// NM_03	0.00112177	3.74289	0.00180006
33	NM_015420	0.000649762	3.73862	0.00232691
34	NM_004804	4.50E-06	3.73311	2.27E-05
35	NM_018407	0.0146217	3.72976	0.00791789
36	NM_018357 /// NM_19795	0.0302604	3.72953	0.00579627
37	NM_001184742 /// NM_00	0.00894066	3.72788	0.0318351
38	NM_199420	1.00E-05	3.71587	9.81E-08
39	NM_018221	0.000469104	3.71319	0.00163048
40	NM_001100620 /// NM_00	0.000114226	3.70764	6.05E-08
41	NM_001005735 /// NM_00	4.65E-05	3.68593	1.23E-06
42	NM_006350 /// NM_01340	0.00125097	3.67947	0.00210039
43	NM_001265589 /// NM_00	0.00115656	3.67733	0.000285786
44	NM_001244949 /// NM_02	0.0203698	3.67562	0.0449126
45	NR_046287 /// NR_046288	7.59E-05	3.66842	0.000292183
46	NM_013388	0.000666656	3.66613	0.00132941
47	NM_004856 /// NM_13855	0.000208324	3.66129	0.000224262

1	NM_005819	0.000763565	3.64823	0.000662148
2	NM_001199649 /// NM_00	0.0071631	3.64413	0.00126765
3	NM_001257137 /// NM_00	0.0001007	3.61911	0.000929619
4	NM_052876	9.22E-06	3.61701	1.55E-05
5	NM_001256849 /// NM_00	0.00244029	3.61364	0.00236615
6	NM_001256185 /// NM_00	0.00405359	3.61167	0.0131277
7	NR_002578 /// NR_002746	0.00179328	3.5859	0.00173266
8	NM_001199981 /// NM_00	0.0022315	3.58393	0.00210703
9	NM_001270452 /// NM_00	0.00256241	3.58208	0.00752918
10	NM_001007239 /// NM_01	0.000654022	3.58025	0.00064355
11	NM_178867 /// NM_21364	0.00412522	3.57936	0.00453457
12	NM_001136039 /// NM_00	0.00654641	3.57469	0.00577675
13	NM_001164623 /// NM_01	0.0011101	3.57295	0.0038238
14	NM_024112	0.00028847	3.55273	0.00119623
15	NM_000048 /// NM_00102	0.00243993	3.55115	0.00827966
16	NM_014047	0.00016116	3.54972	0.000184363
17	NM_001127370 /// NM_00	0.0193097	3.54048	0.0018076
18	NM_006516	0.0106671	3.53324	0.000592474
19	NM_000302	0.00308366	3.52355	0.00770414
20	NM_001163508 /// NM_00	5.94E-05	3.52333	2.88E-05
21	NM_001100819 /// NM_00	0.01127	3.52331	0.0201716
22	NM_152716	1.66E-07	3.50536	7.75E-08
23	NM_004996 /// NM_01986	0.000112803	3.50169	4.92E-06
24	NM_001161580 /// NM_00	0.00104991	3.50164	0.000679653
25	NM_018848 /// NM_17078	0.00463129	3.50042	0.00200076
26	NM_014275 /// NM_05401	0.0206346	3.49152	0.00329981
27	NM_006555	0.000215756	3.49069	0.00135622
28	NM_018944	0.000108524	3.49021	0.000178463
29	NM_018467	0.000144739	3.48105	9.19E-05
30	NM_004544	0.0225121	3.47436	0.0356726
31	NM_016535	0.000302152	3.47319	0.00124492
32	NM_174911	0.0411613	3.46688	0.0370889
33	NM_018683	1.99E-05	3.46322	9.93E-05
34	NM_015420	0.0134292	3.45882	0.0331003
35	NM_001178138 /// NM_00	0.00106433	3.44781	0.000371447
36	NM_001037324 /// NM_00	0.000447193	3.44758	2.80E-05
37	NM_012088	0.000336541	3.4384	0.00168568
38	NM_003594	0.000844199	3.42969	9.07E-05
39	NM_001163817 /// NM_00	2.46E-05	3.42724	1.56E-07
40	NM_001042517 /// NM_00	0.00317186	3.42663	0.00568695
41	NM_030789 /// NM_17858	4.33E-06	3.41915	1.63E-05
42	NM_001008395	0.00018411	3.41671	0.000435812
43	NM_001008222 /// NM_01	0.000478019	3.40444	0.000967503
44	NM_001916	0.0143152	3.40363	0.00118378
45	NM_001150	0.0115668	3.38867	0.0136652
46	NM_000284 /// NM_00117	0.00131395	3.38663	0.00198428
47	NM_022353	0.00676363	3.38459	0.00267575
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1	NM_001846	0.00593924	3.36398	0.0132856
2	NM_001532	9.61E-05	3.36004	7.60E-05
3	NM_001145966 /// NM_00	0.000289329	3.34907	0.000118902
4	NM_002013 /// XR_132760	0.00821376	3.34168	0.0166502
5	NM_014275 /// NM_05401	0.00230893	3.31765	0.00157398
6	NM_001025252 /// NM_00	0.0313241	3.30743	0.0242991
7	NM_018140	0.000390393	3.30506	9.62E-05
8	NM_018086	0.0192802	3.30374	0.00096048
9	NM_002466	0.00120771	3.2807	7.90E-06
10	NM_003388 /// NM_03242	0.000553297	3.27964	0.00102942
11	NM_138348	0.00131764	3.27353	0.00177182
12	NM_152603	0.00514507	3.27021	0.0013994
13	NM_001206774 /// NM_01	0.0109649	3.25535	0.0229978
14	NM_001184891 /// NM_00	0.000115734	3.25179	0.000217532
15	NM_001224 /// NM_03298	0.0148698	3.25024	0.0108862
16	NM_004374	0.0193182	3.23094	0.00432976
17	NM_001253815 /// NM_00	0.0134921	3.22236	0.000191046
18	NM_006558	0.00358896	3.2208	0.00827964
19	NM_001001653 /// NM_05	0.000295956	3.21842	0.000284403
20	NM_144695	0.0006344	3.21764	0.000134017
21	NM_001033505 /// NM_00	3.45E-06	3.21672	1.06E-06
22	NM_001142463 /// NM_00	0.00114118	3.21032	0.00326772
23	NM_001135821 /// NM_00	0.0141858	3.20757	0.00198235
24	NM_001130929 /// NM_01	0.0105507	3.20589	0.00211917
25	NM_153451	0.000614091	3.20157	1.31E-05
26	NM_016456	0.000102669	3.18957	0.000219801
27	NM_001042424 /// NM_00	0.0052781	3.17253	0.0112546
28	NM_138316 /// NM_14897	0.0167124	3.1543	0.00139965
29	NM_005590 /// NM_00559	0.00172831	3.13267	0.00159819
30	NM_005809 /// NM_18173	0.039234	3.12964	0.0206651
31	NM_006499 /// NM_20154	0.0190645	3.12106	0.0170701
32	NM_003255	0.00219103	3.11962	6.15E-05
33	NM_001032292 /// NM_00	0.00172857	3.11864	0.00327552
34	NM_001143990 /// NM_00	0.00342365	3.10646	4.59E-05
35	NM_018353	0.00583957	3.10313	0.00250215
36	NR_028514	0.000174282	3.09571	0.000490317
37	NM_001105562 /// NM_00	5.51E-05	3.09297	0.000165919
38	NM_006451 /// NM_18278	0.0321267	3.06377	0.0411293
39	NM_030811	0.000281967	3.06279	4.76E-05
40	NM_001018073 /// NM_00	1.61E-05	3.05986	3.54E-05
41	NM_018944	0.00299447	3.05795	4.69E-05
42	NM_001039375 /// NM_02	1.10E-05	3.05588	5.25E-06
43	NM_001659	0.0321961	3.04171	0.00273872
44	NM_001258384 /// NM_00	0.00400723	3.03777	0.000419124
45	NM_001145408 /// NM_00	0.00011052	3.02218	0.000134114
46	NR_015366 /// NR_027241	0.0039025	3.01953	0.00220251
47	NM_001142405 /// NM_00	0.00481519	3.0158	6.07E-05

1	NM_001113201 /// NM_00	0.00166535	3.0123	2.94E-05
2	NM_001256686 /// NM_00	0.00294171	3.01074	4.36E-05
3	NM_001204453 /// NM_00	0.00454375	3.00992	0.00327254
4	NM_001166050 /// NM_00	0.00229139	3.00662	0.00347887
5	NM_001033521 /// NM_00	0.00035384	3.00447	0.000143115
6	NM_001047	0.00131137	2.99422	0.000111034
7	NM_018240	0.0055355	2.99391	0.000313931
8	NM_017780	0.00536157	2.99378	0.000449695
9	NM_001188	0.000237903	2.99255	0.000155987
10	NM_000849 /// NR_02453	0.000167988	2.96459	0.000112618
11	NM_001201545 /// NM_02	2.37E-05	2.94882	1.03E-05
12	NM_001199290 /// NM_14	0.00668348	2.93066	0.0013151
13	NM_016074	5.61E-05	2.92846	0.000101123
14	NM_013296	0.000451888	2.92813	0.000118344
15	NR_002785	0.0102791	2.92578	0.000237128
16	NM_001077484 /// NM_03	0.00355477	2.92286	0.00139389
17	NM_001032730 /// NM_03	0.0140734	2.92055	0.0040458
18	NM_001267623 /// NM_03	1.07E-05	2.9203	3.43E-06
19	NM_002936	0.000851502	2.91909	3.62E-05
20	NM_145702	0.0320349	2.91717	0.000122838
21	NM_178448	0.000888349	2.90077	7.16E-06
22	NM_203453	0.0151376	2.88725	0.00558055
23	NM_152699	0.000556353	2.87658	5.01E-05
24	NM_017952	0.0165647	2.86986	0.0141862
25	NM_001024594	0.00966714	2.86602	0.00226845
26	NM_001252641 /// NM_00	0.0121026	2.85767	0.00439137
27	NM_001039589 /// NM_00	0.000562666	2.85665	0.000196377
28	XR_110082 /// XR_112807	0.0112509	2.85571	0.000167397
29	NM_001267608 /// NM_00	4.59E-05	2.84765	6.33E-06
30	NM_005471	0.000387656	2.84327	0.000372697
31	NM_020662	0.0186444	2.84285	0.014838
32	NM_012103 /// NM_18157	0.00881065	2.8407	0.000673517
33	NM_024796 /// NR_02432	0.0213211	2.83935	0.00218459
34	NM_024036	0.00231287	2.82618	0.00157086
35	NM_001033855 /// NM_00	0.00541553	2.81772	0.00149735
36	NM_001177663 /// NM_00	0.00747536	2.80211	0.00319688
37	NM_007059	0.000151459	2.78874	4.24E-05
38	NM_018451 /// NR_04759	0.0111651	2.78487	6.72E-05
39	NM_003258	6.16E-05	2.7837	4.50E-05
40	NM_001008938 /// NM_01	7.71E-05	2.78214	5.96E-05
41	NM_004846 /// XR_112445	0.000351805	2.77611	8.18E-05
42	NM_014607	0.0161466	2.77176	0.00685515
43	NM_001204180	8.18E-06	2.76864	3.07E-09
44	NM_006602 /// NM_08075	0.0120047	2.76808	0.00688017
45	NM_024622	0.0172903	2.75812	0.00265831
46	NM_006014	0.00242948	2.75613	3.22E-06
47	NM_001258384 /// NM_00	0.00322608	2.75029	7.93E-05

1	NM_001013730 /// XR_11C	0.0111702	2.74382	0.00270185
2	NM_032371 /// NM_13841	0.00424538	2.74347	0.000141242
3	NM_006980	0.00285433	2.7377	0.000794649
4	NM_002254	0.00067988	2.73741	0.000111307
5	NM_001130965 /// NM_00	0.00278601	2.7372	0.00025803
6	NM_017813	0.0245251	2.73693	0.00110693
7	NM_000403 /// NM_00100	0.00243563	2.73429	0.00209677
8	NM_000244 /// NM_13079	0.00116467	2.72882	0.000441238
9	NM_001195563 /// NM_00	0.0051406	2.71723	0.00241004
10	NM_012334	0.0134123	2.71605	0.000745807
11	NM_018706	0.00521769	2.70574	0.000153549
12	NM_001190991 /// NM_01	0.00369265	2.68758	4.61E-05
13	NM_001256763 /// NM_01	0.0115766	2.68394	0.00234919
14	NM_015953	0.03592	2.67958	0.01475
15	NM_001015885 /// NM_00	0.000233815	2.67287	3.36E-05
16	NM_032818	0.00147199	2.67203	8.79E-05
17	NM_001098424 /// NM_00	0.0433555	2.65653	0.0305176
18	NM_017646	0.00410256	2.65042	0.000969043
19	NR_024397	0.00496486	2.64975	2.97E-05
20	NM_012293	0.00465933	2.6478	0.000557154
21	NM_001164811	0.017688	2.63661	0.00215088
22	NM_001136033 /// NM_01	0.00584748	2.63507	0.00116982
23	NM_003507	0.0175753	2.63069	6.32E-05
24	NM_001093725	0.000402474	2.62669	3.23E-06
25	NM_015155	0.00493799	2.61596	0.000848966
26	NM_022778	0.00502312	2.61428	0.00267398
27	NM_014426 /// NM_15222	0.0100988	2.61117	0.000130803
28	NM_001025366 /// NM_00	0.00695236	2.60121	0.000133257
29	NM_178229	3.40E-05	2.59576	5.07E-13
30	NM_003258	0.00106387	2.59367	3.31E-06
31	NM_001109903 /// NM_03	0.0012575	2.59044	8.32E-05
32	NM_017927 /// NM_03354	0.00961541	2.58194	0.00566464
33	NM_001002017 /// NM_00	0.000475587	2.57779	0.000147877
34	NM_032371 /// NM_13841	0.0122843	2.57704	0.000372989
35	NM_001099652	0.0260202	2.57227	1.90E-05
36	NM_001130677	0.00466091	2.56175	0.000306874
37	NM_003107	0.0259326	2.55389	0.000636005
38	NM_001247987 /// NM_02	0.0349408	2.55176	3.78E-05
39	NM_001247996 /// NM_01	7.54E-05	2.54405	2.32E-05
40	NM_004442 /// NM_01744	0.00208323	2.54234	3.34E-05
41	NM_001013649	0.0222945	2.53611	0.00302361
42	NM_001204492 /// NM_00	0.0013481	2.52247	6.43E-05
43	NM_001256670 /// NM_00	5.76E-05	2.50841	8.24E-06
44	NM_019070 /// NR_03367	0.000125246	2.50682	1.91E-05
45	NM_033505	0.0122216	2.50652	0.00269497
46	NM_005997	0.0105441	2.49721	0.000441109
47	NM_017927 /// NM_03354	0.0227395	2.48932	0.00208488

1	NM_145231	0.0240059	2.48596	0.00549941
2	NM_001083963 /// NM_00	0.0131973	2.48034	0.000433102
3	NM_001040664 /// NM_00	0.00719132	2.46782	0.000152061
4	NM_004442 /// NM_01744	0.000231369	2.44636	2.24E-05
5	NM_001258384 /// NM_00	0.00525099	2.44141	0.000134695
6	NM_006796	0.00587978	2.42822	0.000496276
7	NM_014426 /// NM_15222	0.00895797	2.40945	0.00234194
8	NM_152341	0.00757604	2.40877	0.000986576
9	NM_001039477 /// NM_00	0.0443508	2.40365	0.0174253
10	NM_003721 /// NM_13444	0.0143483	2.40016	0.00254392
11	NM_018174	0.0289731	2.39212	0.00606325
12	NM_016018 /// NM_02487	0.00547544	2.38855	0.000141053
13	NM_001109938 /// NM_00	0.00994332	2.38565	0.00051123
14	NM_001258033 /// NM_00	0.00680477	2.37989	0.00150437
15	NM_016028 /// NM_01763	0.0241129	2.37215	0.00109897
16	NM_001008491 /// NM_00	0.00794681	2.37142	0.00012502
17	NR_002776	0.00248674	2.35634	0.000118334
18	NM_001198850 /// NM_00	0.00175653	2.35092	0.000179211
19	NM_020386	0.0282001	2.34524	0.00102848
20	NM_000135 /// NM_00101	0.00016353	2.34484	3.49E-06
21	NM_003714	0.0483855	2.34211	0.00522508
22	NM_006579	0.00117407	2.33231	3.11E-06
23	NM_001256574 /// NM_00	0.00700322	2.32804	5.11E-05
24	NM_001015055 /// NM_00	0.0307408	2.32518	2.08E-05
25	NM_019104	0.0372472	2.3192	0.00101841
26	NM_006618	0.0372274	2.31711	0.00197485
27	NM_022477 /// NM_03201	0.00150349	2.31636	0.000143866
28	NM_004567	0.0109774	2.31533	3.30E-05
29	NM_016558 /// NM_03363	0.0205612	2.31225	0.00187022
30	NM_001039477 /// NM_00	0.0349297	2.3087	0.00279409
31	NM_020062	0.047564	2.30708	0.00121847
32	NM_080656	0.00537181	2.30643	0.0010731
33	NM_001257144 /// NM_00	0.00886148	2.3019	1.65E-05
34	NM_001270439 /// NM_00	0.0014331	2.301	6.79E-05
35	NM_025108	0.000179554	2.29448	1.77E-07
36	NM_000135 /// NM_00101	0.00222142	2.28841	8.74E-05
37	NM_001105203 /// NM_00	0.000306743	2.28819	6.11E-08
38	NM_022092	0.0308305	2.28732	2.70E-06
39	NM_006455	0.00239734	2.28175	5.20E-05
40	NM_013432	0.00252919	2.27734	1.45E-05
41	NM_000801 /// NM_00119	0.0181998	2.27205	0.00296202
42	NM_001029991 /// NM_00	0.0281712	2.26914	0.00700075
43	NM_001136035 /// NM_00	0.0458729	2.26895	0.00133049
44	NM_001204364 /// NM_15	0.000360152	2.26129	9.55E-09
45	NM_006943	0.00170733	2.25829	1.18E-05
46	NM_016558 /// NM_03363	0.0180044	2.25449	0.00312224
47	NM_001164391 /// NM_00	0.0202809	2.24901	0.00400399

1	NM_152268	0.00183071	2.2463	7.49E-05
2	NM_001193557 /// NM_02	0.0169498	2.23782	0.000355252
3	NM_004260	0.0114038	2.23154	5.42E-05
4	NM_001166599 /// NM_00	0.0477747	2.22489	0.000377973
5	NM_030625	0.0140239	2.20846	0.000120588
6	NM_001204106 /// NM_00	0.00166686	2.20688	1.90E-05
7	NM_138384	0.0118147	2.19766	0.000285136
8	NM_015327	0.00853369	2.1957	0.00027145
9	NM_005762	0.0110702	2.19206	0.00105357
10	NM_001144002 /// NM_01	0.00637082	2.19038	0.000698744
11	NM_017769	0.0171758	2.18996	0.0011136
12	NM_003797 /// NM_15299	0.0344162	2.18758	0.00194473
13	NM_003740	0.0149678	2.18163	0.000579025
14	NM_001012514 /// NM_00	0.0177222	2.18132	0.00116445
15	NM_006769	0.031934	2.17403	0.00644385
16	NM_006559	0.00071141	2.17389	3.39E-05
17	NM_001039783 /// NM_00	0.00230862	2.15553	0.000123408
18	NM_001145454 /// NM_00	0.000321074	2.14612	5.55E-06
19	NM_001201428 /// NM_01	0.0449453	2.13684	0.00689629
20	NM_004699	0.0435783	2.12711	0.00665859
21	NM_032815	0.000938462	2.11296	6.95E-06
22	NM_013285	0.00518732	2.09976	0.000189222
23	NM_001042631	0.00322677	2.09601	0.000151921
24	NM_000308 /// NM_00112	0.0147243	2.089	0.000470215
25	NM_001018115 /// NM_03	0.0117156	2.08041	1.23E-05
26	NM_001037811 /// NM_00	0.0198788	2.07201	0.000288306
27	NM_001261427 /// NM_00	0.0166277	2.06143	0.000223129
28	NM_173511	0.0101943	2.04909	5.60E-05
29	NM_145012 /// NM_18169	0.0197377	2.04867	0.000169142
30	NM_024112	0.0143324	2.04566	0.00033741
31	NM_001204106 /// NM_00	0.0200284	2.02366	0.00107473
32	NM_194292	0.00847605	2.02179	8.54E-05
33	NM_001085372	0.0135665	2.01606	0.000147273
34	NM_001184977 /// NM_01	0.0143888	2.01505	1.05E-05
35	NM_001099222 /// NM_00	0.00137878	-2.02597	1.84E-05
36	NM_053000 /// NR_015370	0.0445363	-2.03801	0.00525927
37	NM_052900 /// NM_19812	0.043518	-2.03994	0.00306063
38	NM_014867	0.0169534	-2.04477	0.000423071
39	NM_001142685 /// NM_01	0.0154126	-2.04805	0.000194133
40	NM_016353	0.0330585	-2.05208	0.00188074
41	NM_198920	0.0158044	-2.06049	0.000949583
42	NM_000049 /// NM_00112	0.0258824	-2.06347	0.000490738
43	NM_178816 /// NM_20137	0.00677375	-2.06863	5.56E-05
44	NM_001172766 /// NM_00	0.0491818	-2.0928	0.00110792
45	NM_000426 /// NM_00107	0.0156504	-2.09962	2.07E-06
46	NM_024723 /// NM_18292	0.0145025	-2.11112	9.77E-05
47	NM_001168618 /// NM_02	0.0205909	-2.12308	7.38E-05

1				
2	NM_001098402 /// NM_00	0.0309385	-2.12643	0.000148795
3	NM_001005367 /// NM_00	0.00186559	-2.12793	8.63E-05
4	NM_000426 /// NM_00107	0.0107995	-2.13707	8.13E-07
5	NM_000418 /// NM_00100	0.0485917	-2.13971	0.00371708
6	NM_020734	0.0185038	-2.14185	0.00112458
7				
8	NM_001256732 /// NM_00	0.00103473	-2.14745	4.09E-05
9	NM_001029851 /// NM_00	0.0251409	-2.15436	1.30E-05
10	NM_170710 /// NM_18126	0.0379251	-2.15487	5.69E-06
11				
12	NM_001136472 /// NM_00	0.0483293	-2.16212	3.13E-05
13	NM_080283 /// NM_17238	0.00169874	-2.18976	5.88E-05
14	NM_001128432 /// NM_02	0.00646131	-2.20278	0.000260008
15	NM_178499	0.0220811	-2.2066	0.00422569
16				
17	NM_001169109 /// NM_00	0.0294738	-2.21427	1.32E-06
18	NM_001015045 /// NM_00	0.00677561	-2.22016	4.94E-05
19	NM_001031687 /// NM_00	0.0244229	-2.23129	0.000490266
20	NM_004613 /// NM_19895	0.022703	-2.23957	0.000120943
21				
22	NM_002373	0.0010806	-2.24885	7.70E-05
23	NM_001195535	0.000156656	-2.26989	1.39E-07
24	NM_001127235 /// NM_00	0.0381493	-2.27382	0.0111832
25	NM_001144960	0.00386188	-2.275	0.000294867
26				
27	NM_002919 /// NM_13442	0.0335753	-2.27714	3.68E-05
28	NM_001166693 /// NM_00	0.00202331	-2.28203	4.23E-06
29	NM_001111038 /// NM_14	0.00484257	-2.28782	1.97E-05
30				
31	NM_030821	0.0248973	-2.28897	0.000871953
32	NM_001077181 /// NM_00	0.0472355	-2.30253	0.00393145
33	NM_001032287 /// NM_00	0.00428576	-2.30859	0.000253767
34	NM_001003789 /// NM_00	0.0124339	-2.31234	0.000465315
35				
36	NM_001269053 /// NM_13	0.0227174	-2.31379	0.00162138
37	NM_001025105 /// NM_00	0.0392068	-2.31504	0.00222511
38	---	0.0276852	-2.32064	0.00404862
39	NR_036487	0.0305442	-2.32463	0.00148852
40				
41	XM_001125684	0.00783062	-2.33546	0.000976223
42	NM_001256732 /// NM_00	0.00285295	-2.33693	0.000359917
43	NM_000389 /// NM_00122	0.0299391	-2.34269	4.22E-07
44	NM_001195639 /// NM_05	0.00606997	-2.35306	0.000885814
45				
46	NM_002912	0.0117839	-2.38068	0.00037981
47	NM_001116	0.0490926	-2.38476	0.00257178
48	NM_000668	0.00351059	-2.38644	0.00054212
49	NM_152723	0.0396672	-2.38693	0.0116277
50				
51	NM_017655	0.0282523	-2.40463	0.0076759
52	NM_001199096 /// NM_00	0.000267241	-2.40938	4.85E-05
53	NM_016441	0.0364096	-2.42288	0.00586934
54	NM_001008710 /// NM_00	0.0110631	-2.42486	0.00385031
55				
56	NM_003263	0.00142513	-2.42533	4.38E-05
57	NM_005761 /// NR_03768	0.00496711	-2.43864	0.000153534
58	NM_020676	0.00019809	-2.4402	2.64E-07
59	NM_001105248 /// NM_00	0.00783602	-2.45457	0.000567958
60				

1	NM_001031715 /// NM_02	0.0266489	-2.46802	0.00316198
2	NM_001134405 /// NM_00	0.0100258	-2.47406	0.00146619
3	NM_014057 /// NM_02441	0.00468197	-2.47425	0.00104327
4	NM_000476	2.48E-05	-2.4743	4.17E-07
5	NM_005228 /// NM_20128	0.0429253	-2.47705	0.0230957
6	NM_001251977 /// NM_00	0.0186661	-2.48141	0.00302333
7	NM_018956	0.000107207	-2.49192	6.00E-06
8	NM_001039590 /// NM_00	0.00425431	-2.49309	1.03E-05
9	NM_019604	0.00639602	-2.49351	0.0023804
10	NM_001099337 /// NM_14	0.0206813	-2.5002	0.00611079
11	NM_001001687 /// NR_02	0.010509	-2.50077	0.00198774
12	NR_015430	0.00109188	-2.50098	0.000305252
13	NM_153228	0.00449995	-2.50312	0.000588123
14	NM_001100875 /// NM_15	0.000765126	-2.50893	3.10E-05
15	NM_001039395 /// NM_01	0.00152194	-2.50963	6.32E-05
16	NM_001045	0.000742975	-2.51447	3.88E-05
17	NM_001190918 /// NM_00	0.000171788	-2.5154	2.71E-05
18	NM_016617	0.00885548	-2.54424	0.00294288
19	NM_016270	0.000297541	-2.56933	1.41E-05
20	NM_001003819 /// NM_00	0.00110773	-2.56968	0.000112429
21	NM_001015045 /// NM_00	0.0248591	-2.56976	0.0019299
22	NM_003012	0.00378275	-2.57452	0.00011459
23	NM_017633	0.0385296	-2.58067	7.68E-05
24	NM_001102426 /// NM_00	0.00961539	-2.58276	0.000865543
25	NR_038854	0.00241636	-2.59563	5.34E-05
26	NM_001039210 /// NM_00	0.00893351	-2.60249	7.77E-05
27	---	0.00398051	-2.60315	3.03E-06
28	XR_108755 /// XR_110657	0.00133221	-2.60334	1.88E-05
29	NM_000611 /// NM_00112	0.00420863	-2.60752	1.24E-05
30	NM_001145307 /// NM_00	0.0120613	-2.60864	0.00111323
31	NM_144653	0.0465689	-2.61154	0.00848512
32	NM_001969 /// NM_18300	0.0051714	-2.6191	0.00011993
33	NM_001122824 /// NM_00	0.0124609	-2.61958	4.25E-08
34	NM_000130	0.0267263	-2.62511	0.000625744
35	NM_015254	0.0114919	-2.63245	0.000649405
36	NR_001564	0.02612	-2.63685	0.0013639
37	NM_003079	0.000392276	-2.6371	9.73E-05
38	NM_001199922 /// NM_01	0.00494102	-2.63724	0.00203778
39	NM_000813 /// NM_02191	0.0179987	-2.64001	0.00938966
40	NM_001014979 /// NM_00	0.0306526	-2.64307	0.00244117
41	NM_014510 /// NM_03302	0.035616	-2.64545	0.0161402
42	NM_007231	0.0196991	-2.64765	0.00516841
43	NM_001077269 /// NM_00	0.0414693	-2.6501	0.00424409
44	NM_052929	0.000837951	-2.65631	0.00024625
45	NM_152517	0.0298479	-2.65969	0.0153386
46	NM_032606	0.00167317	-2.66027	0.000430781
47	NR_038199 /// NR_038200	0.000972902	-2.66277	7.25E-05

1	NM_001039395 /// NM_01	0.00624734	-2.6687	0.00375484
2	NM_000301 /// NM_00116	0.00994969	-2.66885	0.000458617
3	NM_016441	0.0102492	-2.67181	0.000215359
4	NM_017637	0.0038799	-2.68319	0.000316738
5	NM_006197	0.0285099	-2.68429	0.000695191
6	NM_001003799 /// NM_00	0.00183597	-2.68533	0.000220236
7	NM_207361	0.0128581	-2.68703	7.06E-05
8	NM_207317	0.00242821	-2.68784	0.000246677
9	NR_029598	0.0303698	-2.69971	0.0192733
10	NM_001177660 /// NM_00	0.00941352	-2.70221	0.00638033
11	NM_015687	0.00821967	-2.7089	0.00199869
12	NM_018672 /// NM_17223	0.00212933	-2.71344	0.000106954
13	NM_001128166 /// NM_00	0.0295043	-2.71892	0.0001756
14	NM_001129889 /// NM_00	0.00974221	-2.7366	0.000453927
15	NM_002612	0.00988604	-2.74059	0.00303132
16	NM_001996 /// NM_00648	0.00331138	-2.75126	0.000647835
17	NM_001145678 /// NM_17	0.000605818	-2.75864	0.00015825
18	NM_000052	0.0326828	-2.7616	0.0130274
19	NM_001650 /// NM_00402	0.0014983	-2.76213	0.000176097
20	NM_001252385 /// NM_00	0.00967559	-2.76658	0.00500005
21	NM_001204087 /// NM_00	0.0120163	-2.76838	0.00290836
22	NM_001130110 /// NM_01	0.0383273	-2.78419	0.00549803
23	NM_005801	0.00117396	-2.78552	8.32E-05
24	NM_000519	0.00424332	-2.79981	0.00194246
25	NM_001003794 /// NM_00	0.0129039	-2.80885	0.00154537
26	NM_001169117 /// NM_00	0.00034273	-2.80947	1.25E-06
27	NM_032269	0.00379675	-2.81194	0.00215773
28	NM_001256732 /// NM_00	0.00825622	-2.81518	0.00245099
29	NM_021958	0.028298	-2.82016	0.00635712
30	NM_016422	0.00011115	-2.82363	2.15E-05
31	NM_001204126 /// NM_00	0.000210152	-2.82394	5.98E-05
32	NM_001006641 /// NM_00	0.00181043	-2.83028	1.51E-05
33	NM_139265	0.00501849	-2.83173	5.14E-05
34	NM_002269	0.0378815	-2.8332	0.00332278
35	NM_002185	0.00943708	-2.83422	0.00319312
36	NM_001145670 /// NM_00	0.0291515	-2.83633	0.00250088
37	NM_018306	0.000595363	-2.83838	2.64E-05
38	NM_181426	0.00722633	-2.84441	0.000126199
39	NM_017637	0.00274599	-2.84535	0.000880937
40	NM_000878	2.08E-05	-2.84641	2.79E-05
41	NM_001031737 /// NM_17	0.00461125	-2.84676	6.41E-05
42	NM_001013676 /// NM_02	0.000303016	-2.86882	4.37E-05
43	NM_001032282 /// NM_00	0.0396145	-2.87439	0.0017656
44	NM_016262	0.00803666	-2.87767	0.00588235
45	NM_001122824 /// NM_00	0.0010784	-2.88073	4.78E-08
46	NM_001039724 /// NM_00	0.00508191	-2.88525	0.00263463
47	NM_001135608 /// NM_01	0.0402685	-2.89288	0.00273028

1	NM_001130159 /// NM_00	0.00456499	-2.90248	0.00210967
2	NM_032853 /// NR_024241	0.000129613	-2.9032	8.10E-05
3	NM_001009607 /// NM_00	0.00351253	-2.90567	0.00173373
4	NM_001100818 /// NM_01	0.0053009	-2.91369	0.00111809
5	NM_001256054 /// NM_01	0.00101828	-2.91575	0.000788957
6	NM_000167 /// NM_00112	0.00322117	-2.9168	6.55E-07
7	NM_000457 /// NM_00103	0.00048928	-2.91817	0.000110972
8	NM_001136021 /// NM_00	0.00293569	-2.928	2.43E-05
9	NM_001024683 /// NM_14	0.00220323	-2.92996	0.00297169
10	NM_001171581 /// NM_00	0.000858676	-2.93026	6.51E-05
11	NM_001066	0.000345323	-2.93921	0.000573525
12	NM_001175	0.00140092	-2.94108	0.00214931
13	NM_001134673 /// NM_00	0.0181315	-2.94696	0.0175473
14	NM_144965	0.00234123	-2.94736	0.00105662
15	NM_152572	0.000298359	-2.94925	0.000142115
16	NM_152519	0.00113734	-2.95148	0.000275563
17	NM_003884	0.0111061	-2.96145	0.000284311
18	NM_001007022 /// NM_00	0.0003816	-2.96489	6.71E-06
19	NM_001142649 /// NM_21	0.000420318	-2.96577	0.00017049
20	NR_015377 /// NR_047570	0.000700644	-2.97597	5.74E-05
21	NM_182520	1.96E-06	-2.97823	5.31E-07
22	NM_001015045 /// NM_00	0.0121261	-2.97912	0.00129819
23	NM_031437 /// NM_18266	0.023144	-2.99119	0.00190643
24	NM_015335	0.00754516	-2.99327	0.0059581
25	NM_145208	5.91E-05	-2.99634	1.94E-05
26	NM_001166271 /// NM_15	0.00193795	-2.99659	0.00021692
27	NM_001085399 /// NM_00	0.010774	-3.01618	0.000933156
28	NM_001136021 /// NM_00	0.0013851	-3.01902	1.20E-05
29	NM_004786 /// NR_024546	0.00515752	-3.01996	1.38E-06
30	NM_001199942 /// NM_01	0.000217755	-3.02883	8.37E-05
31	NM_005228 /// NM_20128	0.00448466	-3.03582	0.000156312
32	NM_001033578 /// NM_00	0.00685404	-3.04223	0.00176308
33	NM_000426 /// NM_00107	0.00565174	-3.04494	2.32E-06
34	NM_001042479 /// NM_00	0.00311048	-3.04686	0.00311775
35	NM_030666	0.00650493	-3.04938	9.68E-07
36	NM_001079529 /// NM_00	0.00017506	-3.04956	0.000138
37	NR_026867	0.0109684	-3.04998	0.000785492
38	NM_001129993 /// NM_03	0.011193	-3.05924	0.000644653
39	NM_152704 /// NM_19913	0.00397975	-3.05925	0.000843482
40	NM_001130957 /// NM_00	0.00830186	-3.07207	0.0106817
41	NM_001134830 /// NM_00	2.36E-05	-3.08181	1.69E-07
42	NM_030775 /// NM_03264	1.52E-05	-3.08196	3.26E-05
43	NM_144644	0.00404509	-3.0831	0.000340853
44	NM_033124	0.000123891	-3.08596	8.70E-05
45	NM_022140	0.00259995	-3.10145	0.00512274
46	NM_014859	0.020009	-3.10382	0.0208398
47	NM_000668	0.0185201	-3.11793	0.0022059

1	NM_000601 /// NM_00101	0.00394823	-3.12115	1.69E-05
2	NM_001267562 /// NM_00	0.0088958	-3.13076	0.00267395
3	NM_001080394 /// XM_00	4.86E-05	-3.13445	0.000141967
4	NM_001008534 /// NM_00	0.0112258	-3.13508	0.00386532
5	NR_003521 /// NR_026589	0.000591117	-3.14262	0.000312748
6	NM_024882 /// NR_02680	0.00287234	-3.15	0.0064445
7	NM_001033604 /// NM_00	0.0380569	-3.15085	0.00330918
8	NM_152632	0.000802097	-3.15375	0.000493507
9	NM_030666	0.00424478	-3.15464	2.16E-06
10	NM_004951	0.00304145	-3.16045	0.00353457
11	NM_000611 /// NM_00112	0.00096279	-3.1758	0.000667196
12	NM_004980 /// NM_17219	0.000846114	-3.1766	0.000244791
13	NM_198081	0.000166141	-3.17723	0.000100238
14	NM_001139466 /// NM_00	0.0232921	-3.17788	0.0364624
15	NM_001100411 /// NM_02	0.000864397	-3.17794	0.000108671
16	NM_004155	0.0113908	-3.18038	0.0140242
17	NM_198275	0.00023492	-3.1998	2.71E-05
18	NM_000705	0.00376374	-3.20084	0.000139447
19	NM_058180 /// NM_19907	0.00479704	-3.20865	0.00428441
20	NM_000926 /// NM_00120	0.0259025	-3.20954	0.0377844
21	NM_022121	0.0356953	-3.21674	0.0348304
22	NM_001172420 /// NM_01	0.00446361	-3.22062	3.08E-05
23	NM_001242702 /// NM_17	0.0217416	-3.22081	0.0153753
24	NM_033225	0.00138195	-3.22701	0.000146969
25	NM_001178003 /// NM_14	5.92E-05	-3.22772	2.06E-08
26	NM_001173461 /// NM_00	0.000107385	-3.22909	7.51E-06
27	NM_001401 /// NM_05715	0.00374625	-3.2303	2.09E-05
28	NM_001137550 /// NM_00	0.00195512	-3.23155	0.00243561
29	NM_138801	0.00528187	-3.23723	0.000758501
30	NM_020707 /// NR_02775	5.41E-05	-3.239	2.88E-05
31	NM_017425	0.0392738	-3.24297	3.35E-05
32	NM_203454	0.00158472	-3.25377	7.56E-05
33	NM_001010922 /// NM_00	0.0011035	-3.25741	0.00140152
34	NM_004840	0.00264063	-3.26134	0.000489614
35	NM_001079530 /// NM_03	4.12E-05	-3.26591	3.37E-05
36	XM_001716232 /// XM_00	1.79E-05	-3.26749	9.09E-06
37	NM_018702	0.000109457	-3.26897	5.60E-05
38	NM_018699	0.0323911	-3.27198	0.000113896
39	NM_004048	0.013988	-3.27337	0.00857054
40	NM_001149 /// NM_00120	0.019022	-3.27471	0.0232108
41	NM_001008710 /// NM_00	0.0100137	-3.2776	0.00288906
42	NM_181645	0.00168888	-3.28837	0.000674568
43	NM_021148 /// NM_03354	0.00157171	-3.29685	7.27E-05
44	NM_001197237 /// NM_00	3.90E-05	-3.29971	9.75E-05
45	NM_001256370 /// NM_02	0.0088917	-3.30424	0.0217077
46	NM_033063 /// NM_20757	4.70E-05	-3.30659	2.01E-05
47	NM_001129889 /// NM_00	3.50E-05	-3.31719	3.59E-05

1	NM_018010	0.00116117	-3.31723	2.71E-05
2	NM_002121	9.07E-06	-3.32203	7.73E-06
3	NM_001011513 /// NM_00	0.0203459	-3.32685	0.000580662
4	NM_001256536 /// NM_00	0.000708269	-3.33509	0.00116863
5	NM_001647	0.0030668	-3.33526	0.00020798
6	NM_007085	0.000355892	-3.33752	0.001463
7	NM_001100390 /// NM_15	0.00446949	-3.33956	0.0134469
8	NM_001207062 /// NM_03	0.000873227	-3.34017	3.31E-06
9	NM_015566 /// NR_04646	0.0149607	-3.34682	0.0221374
10	NM_001099951 /// NM_00	5.88E-05	-3.34861	2.76E-05
11	NM_178816 /// NM_20137	0.0045263	-3.35791	9.36E-05
12	NM_001199739 /// NM_00	0.000141591	-3.35795	7.95E-07
13	NM_001080463 /// NM_00	0.0330049	-3.36902	0.0109904
14	NM_000518	0.0145901	-3.37492	0.004776
15	NM_031442	0.00260268	-3.37879	0.000741198
16	NM_000416	4.98E-05	-3.38111	3.21E-06
17	NM_001199377 /// NM_01	0.00202949	-3.38528	8.50E-05
18	NM_003630	0.0027804	-3.38626	0.00567663
19	NM_001035230 /// NM_00	0.000832587	-3.38659	0.00243662
20	NM_003956	0.00214063	-3.3921	0.000404266
21	NM_031453	0.0453984	-3.39464	0.0313315
22	NM_004278	3.05E-05	-3.40219	8.21E-05
23	NM_001178145 /// NM_00	0.00211059	-3.40388	0.00326104
24	NM_001162997	0.000295133	-3.40432	8.12E-05
25	NM_014620 /// NM_15363	0.0150421	-3.41035	0.0191084
26	NM_181726	0.0038657	-3.41118	8.50E-05
27	NM_144682	0.0335177	-3.41287	0.0358805
28	NM_001025076 /// NM_00	0.013983	-3.41539	6.84E-05
29	NM_152765	0.000849764	-3.42442	0.00346325
30	NM_000512	9.76E-05	-3.42695	0.000302988
31	NM_001242779 /// NM_00	0.0317056	-3.43849	0.0155649
32	NM_004166 /// NM_00416	0.00720889	-3.45609	0.00062594
33	NM_000301 /// NM_00116	0.00155289	-3.45728	0.000151773
34	NM_001964	0.0247923	-3.45994	0.000316296
35	NM_001195291 /// NM_00	0.0127545	-3.46945	0.0297
36	NR_029389 /// NR_029390	0.000654931	-3.47246	0.00322143
37	NM_012307	2.17E-06	-3.48046	3.57E-07
38	NM_001034191 /// NM_00	0.00656107	-3.48352	0.00406649
39	NM_001008781	0.00311046	-3.48437	0.0111454
40	NM_152376	0.000357613	-3.49372	0.000482243
41	NM_001039801 /// NM_00	0.0103598	-3.49514	0.0162399
42	NM_018650	0.00141554	-3.50388	0.000572068
43	NM_001177704 /// NM_14	4.61E-05	-3.50469	0.000187852
44	NM_001142314 /// NM_08	0.0011214	-3.50519	0.000501277
45	NM_017801	0.011319	-3.5113	0.0102829
46	NM_001969 /// NM_18300	0.00973001	-3.51383	0.0183932
47	NM_001251977 /// NM_00	0.00359696	-3.53196	0.00186449

1				
2	NM_015312 /// NM_03220	0.000415735	-3.5361	0.000672093
3	NM_001017397 /// NM_00	0.0243885	-3.54055	0.00229668
4	NM_001039772 /// NM_00	0.0419386	-3.54504	0.000174081
5	NM_001372 /// NM_00466	0.000175006	-3.54821	5.43E-07
6	NM_005368 /// NM_20337	0.000144167	-3.55225	0.000112826
7	NM_178816 /// NM_20137	0.000154848	-3.55609	0.000427459
8	NM_001100397 /// NM_00	0.00257821	-3.56029	0.000654504
9	NM_001007022 /// NM_00	0.00814151	-3.56306	0.00247264
10	NM_017637	0.0100937	-3.56969	0.0227163
11	NM_001113178 /// NM_00	0.0201723	-3.58225	0.025003
12	NM_021615	0.00557804	-3.58708	0.0021837
13	NM_001243961 /// NM_00	0.000259872	-3.59629	0.000388517
14	NR_029396	0.00112966	-3.59629	4.38E-05
15	NR_024398	0.000137823	-3.61354	1.35E-05
16	NM_003894 /// NM_02281	0.00450866	-3.62286	0.000278931
17	NM_001200049 /// NM_01	6.07E-08	-3.62376	3.39E-08
18	NM_016608	0.00085506	-3.62992	0.000789793
19	NM_002734 /// NM_21247	0.000269988	-3.64053	0.000206759
20	NM_183376	0.0201581	-3.65633	0.00326503
21	NM_001040113 /// NM_00	0.00994108	-3.65953	0.00119562
22	NM_001080836	0.000249789	-3.66065	4.68E-05
23	NM_001033024 /// NM_00	1.74E-05	-3.66445	0.000215923
24	NM_006255	0.0020497	-3.66812	0.0112418
25	NM_001204197 /// NM_01	0.00864645	-3.66881	3.84E-07
26	NM_016010	0.00493807	-3.66998	0.000297791
27	NM_001143676 /// NM_00	0.0138485	-3.68213	0.0013566
28	NM_000813 /// NM_02191	0.00264215	-3.68318	0.00356944
29	NM_006762	0.0111879	-3.68501	0.0184213
30	NM_021179	0.0247234	-3.68944	4.59E-05
31	NM_001199149 /// NM_00	0.0141214	-3.68965	0.0333333
32	NM_015896	0.00123314	-3.69089	0.00511284
33	NM_001178044 /// NM_00	0.00945536	-3.69359	0.0088899
34	NM_025055 /// NM_18279	7.42E-06	-3.70033	2.32E-06
35	NM_001165 /// NM_18296	0.0299424	-3.70181	1.05E-05
36	NM_001767	0.00191039	-3.7071	0.00603769
37	NM_001080556 /// NM_14	0.00138298	-3.712	8.72E-05
38	NM_001173463 /// NM_00	0.00497476	-3.71624	3.82E-06
39	NM_001161661 /// NM_00	0.00128661	-3.71684	0.00103746
40	NR_024461 /// NR_024462	0.00881733	-3.72767	0.0175482
41	NM_001242359 /// NM_01	0.00479063	-3.73799	0.00942075
42	NM_001193300 /// NM_00	0.0142174	-3.74026	0.0351122
43	NM_000814 /// NM_00119	0.000198683	-3.74847	2.07E-05
44	NM_001134830 /// NM_00	0.000369873	-3.75242	0.000149332
45	NM_001007022 /// NM_00	0.00450849	-3.75487	0.000341879
46	NM_014433	0.000597239	-3.76579	8.13E-05
47	NM_001253835 /// NM_00	1.30E-05	-3.77893	4.36E-06
48	NM_000880 /// NM_00119	0.00377308	-3.78221	1.56E-06

1	NM_001146694 /// NM_00	2.74E-05	-3.78383	0.0001478
2	NM_001010922 /// NM_00	6.42E-05	-3.78755	5.56E-06
3	XR_039953 /// XR_039955	0.00108855	-3.78984	2.88E-05
4	NM_001161572 /// NM_00	0.00614284	-3.79587	0.000336678
5	NR_038244 /// NR_038245	0.00192196	-3.80404	0.000668548
6	NM_001134649 /// NM_00	0.00505014	-3.8134	0.0244049
7	NM_022128	0.0021416	-3.81647	0.00661999
8	NM_000328 /// NM_00102	0.0154027	-3.81725	0.0392009
9	NM_153838	0.0108547	-3.81755	0.0108156
10	NM_152357	0.00336564	-3.82066	0.00163243
11	NM_054017 /// NR_026814	0.00151254	-3.82821	9.23E-05
12	NM_152511	0.00180342	-3.84185	0.000163325
13	NM_001964	0.0156642	-3.84403	8.92E-07
14	NM_001142315 /// NM_00	0.0164218	-3.84569	0.0352312
15	NM_001018046 /// NM_02	0.000154019	-3.86003	0.00012962
16	NM_173528	0.000612077	-3.86005	7.13E-05
17	NM_152550	0.0022749	-3.86274	0.00182443
18	NM_001143943 /// NM_03	0.0305517	-3.86321	0.00654536
19	NM_001161575 /// NM_01	4.79E-06	-3.87237	5.68E-07
20	NM_020817	0.00179929	-3.87281	0.0002602
21	NM_014510 /// NM_03302	0.00244303	-3.88575	0.00047226
22	NM_025228	0.000293792	-3.89512	0.000839743
23	NM_033063 /// NM_20757	4.63E-05	-3.8998	2.72E-06
24	NM_001100590 /// NM_01	0.00158276	-3.90781	0.00894831
25	NM_001223 /// NM_00125	0.000115027	-3.91012	0.000582117
26	NM_001039940 /// NR_01	0.00680392	-3.91527	0.000583579
27	NM_006981 /// NM_17319	0.00123657	-3.93549	0.000178151
28	NM_001172420 /// NM_01	0.000423173	-3.93725	0.00346757
29	NM_001204126 /// NM_00	0.000420319	-3.93902	0.000379478
30	NM_016010	0.0034536	-3.95383	0.00722535
31	NM_152696 /// NM_18135	2.69E-05	-3.95853	3.32E-06
32	NM_152519	0.00291701	-3.96173	4.50E-05
33	NM_001039350 /// NM_00	1.93E-05	-3.9661	0.000268673
34	NR_033852	0.000649266	-3.97421	0.00381958
35	NM_006988	0.00477187	-3.99349	0.00551778
36	NM_173496	0.00996594	-3.9945	0.0472841
37	NM_153606	0.000413434	-3.99712	8.10E-05
38	NM_024763 /// NM_20701	0.00439377	-3.99745	0.002315
39	XR_109003 /// XR_111042	5.25E-05	-4.00473	0.000362208
40	NR_038366 /// NR_038367	0.047945	-4.01447	0.00193089
41	XR_108924 /// XR_113209	0.000137848	-4.01881	1.33E-06
42	NM_000508 /// NM_02187	0.00332756	-4.02066	0.000891281
43	NM_018952 /// NM_15603	0.0375519	-4.02514	0.00658601
44	NM_001199096 /// NM_00	1.90E-05	-4.02637	9.47E-05
45	NM_021199	0.00100131	-4.02843	3.57E-05
46	NM_207307	0.00213771	-4.03458	0.00160178
47	NM_001134435 /// NM_03	0.0217994	-4.03818	0.000243271

1	NM_001007224 /// NM_00	0.000848599	-4.03941	0.00566033
2	NM_001040092 /// NM_00	0.0018771	-4.03981	0.000276799
3	NM_001031804 /// NM_00	0.000240587	-4.04146	0.000477452
4	NM_001030287 /// NM_00	0.000173567	-4.04687	0.00118708
5	NM_001082537 /// NM_00	1.97E-05	-4.06342	2.13E-05
6	NM_002163	0.000280131	-4.06471	0.000554786
7	NR_038897	0.00498786	-4.07033	0.011337
8	NM_024633 /// NR_026779	0.00759523	-4.07282	0.0194724
9	NM_001206960 /// NM_00	0.00180835	-4.07635	0.00375501
10	NM_018409	0.00593832	-4.09675	0.00138488
11	NM_006531 /// NM_17560	4.69E-05	-4.10484	1.15E-05
12	NM_000204	0.00177877	-4.10727	2.16E-05
13	NM_001736	2.93E-05	-4.11051	3.87E-06
14	NM_022785 /// NM_19885	3.15E-06	-4.11285	5.22E-07
15	NM_017434 /// NM_17594	0.00504833	-4.11949	0.00798345
16	NM_001126328 /// NM_03	0.0117871	-4.13137	0.0468996
17	NM_001014440	9.89E-06	-4.13357	3.10E-05
18	NM_001195683 /// NM_00	0.0068883	-4.14628	0.00766548
19	NM_032853 /// NR_024241	0.00262557	-4.14642	0.00396288
20	NM_138796	0.0273343	-4.14644	0.00123497
21	NM_006564	0.00240549	-4.14822	0.000726243
22	NM_032133	7.81E-05	-4.16062	8.73E-05
23	NM_000248 /// NM_00118	0.0183501	-4.16517	0.000773652
24	NM_005195	0.00118888	-4.16947	0.0027669
25	NM_001025076 /// NM_00	0.000168216	-4.17211	0.0034968
26	NM_001025194 /// NM_00	0.00143876	-4.17721	0.000399282
27	NM_178824	0.00166726	-4.17795	0.00181512
28	NM_001135099 /// NM_00	0.00427933	-4.18107	0.000323968
29	NM_000596 /// NM_00101	0.000397351	-4.18808	3.76E-05
30	NM_005668 /// NM_17505	0.00302595	-4.19683	0.00167188
31	NM_173554	0.00563538	-4.20916	0.000500207
32	XR_109642 /// XR_112116	0.00104287	-4.21005	0.000268213
33	NR_002819 /// XR_110915	0.00239333	-4.21338	0.019941
34	NM_001168499 /// NM_01	3.61E-05	-4.22583	0.000124703
35	NM_005611	2.69E-05	-4.2301	6.60E-05
36	NM_175900	0.00263091	-4.23259	0.00108411
37	NM_001163417 /// NM_00	0.00252009	-4.2336	0.0139
38	NM_020307	0.00185241	-4.2411	0.0068424
39	NM_006269	0.000437974	-4.24321	8.52E-05
40	NM_005544	0.00218874	-4.24731	0.00284154
41	NM_001177701 /// NM_00	7.98E-06	-4.25722	1.26E-05
42	NM_033027	0.00226471	-4.26077	0.000343716
43	NM_001144763 /// NM_00	8.06E-06	-4.27037	0.000147844
44	NM_000301 /// NM_00116	4.58E-05	-4.27732	7.87E-06
45	NM_145053	4.07E-06	-4.27899	0.000104821
46	NM_014648	0.00204576	-4.28227	0.00029375
47	NM_000130	0.00258617	-4.28251	0.000106146

1	NM_014365	7.15E-05	-4.28681	3.08E-06
2	NM_001243965 /// NM_00	0.0318305	-4.31677	0.0197362
3	NM_001100396 /// NM_17	6.79E-08	-4.32014	7.98E-07
4	NM_001256113 /// NM_17	0.000416623	-4.32357	7.75E-06
5	NM_002032	0.00754486	-4.33418	0.039198
6	NM_004787	0.0100181	-4.34279	0.0190241
7	NM_001135598 /// NM_15	0.00568462	-4.34445	0.010658
8	NM_001130142 /// NM_01	0.000705083	-4.34749	4.42E-05
9	NM_002966	0.00847192	-4.34806	1.62E-05
10	NM_001127391 /// NM_13	0.00285967	-4.35209	0.00100155
11	NM_001098504 /// NM_00	0.00551148	-4.35362	0.00102084
12	NM_001194999 /// NM_00	0.000441865	-4.35844	0.00155664
13	NM_001039570 /// NM_03	0.000696121	-4.36018	0.00572805
14	NM_016441	0.013683	-4.36385	0.026032
15	NM_004841 /// NM_17069	0.000741931	-4.36991	0.00671701
16	NM_020980	0.000176838	-4.37247	0.00173405
17	NR_046241	0.000743327	-4.38519	0.00321328
18	---	0.000568013	-4.38789	0.000489016
19	NM_001040712 /// NM_00	0.00659747	-4.39742	0.00657142
20	NM_001079529 /// NM_00	0.000227811	-4.39869	8.43E-05
21	NM_001122769 /// NM_18	0.000734562	-4.40031	7.21E-06
22	NM_001243093 /// NM_00	0.000221426	-4.40242	6.64E-05
23	NM_017439	0.00544977	-4.40343	0.0022404
24	NM_001199640 /// NM_00	0.00046527	-4.40531	5.37E-08
25	NM_001130159 /// NM_00	7.92E-05	-4.40545	0.0017668
26	NM_006682	0.00585273	-4.41054	0.0064113
27	NM_001243965 /// NM_00	0.0223145	-4.41088	0.0116216
28	NM_004344	0.00275518	-4.42394	0.000540416
29	NM_004538	0.000410356	-4.43366	0.00842909
30	NM_001018039 /// NM_00	0.00210709	-4.4344	5.59E-05
31	NM_018168	0.0107874	-4.4398	8.43E-08
32	NM_014887 /// NM_03311	0.00118353	-4.44934	0.00155703
33	NM_001127391 /// NM_13	0.000412616	-4.45328	0.000396085
34	NM_001130156 /// NM_00	0.00579406	-4.46711	0.0218211
35	NM_001099289	0.000546782	-4.46982	0.00138534
36	NM_001105659 /// NM_14	3.93E-06	-4.47073	0.000277334
37	NR_003521 /// NR_026589	0.00219101	-4.47254	0.00845802
38	NM_001139490 /// NM_01	0.00133672	-4.48158	0.00113077
39	NM_138444	0.0426204	-4.48217	0.00336347
40	NM_024806 /// NM_19912	0.000123573	-4.48888	5.05E-05
41	NM_181644	0.00164057	-4.49092	0.00458706
42	NM_000109 /// NM_00400	0.00873171	-4.49839	7.05E-07
43	NM_015566 /// NR_046462	0.0042281	-4.50888	0.0152266
44	NM_005544	0.040968	-4.5134	0.0339986
45	NM_001145313 /// NM_03	0.0141924	-4.51538	0.00144847
46	NM_182493	8.30E-06	-4.51563	8.76E-08
47	NM_138788	0.000107587	-4.52313	0.00029853

1				
2	NM_152704 /// NM_19913	0.00214423	-4.52423	0.000154216
3	NM_001039348 /// NM_00	0.0293705	-4.52677	6.41E-05
4	NM_019073	0.0109566	-4.53936	0.0010202
5	NM_001145670 /// NM_00	0.000447981	-4.54006	0.000864111
6	NM_001077416 /// NM_00	0.00392957	-4.54508	5.67E-05
7	NM_001135863 /// NM_00	2.49E-05	-4.54881	0.000351053
8	NM_001163075	1.97E-05	-4.5707	0.000468791
9	NM_001170690 /// NM_02	0.000703496	-4.57132	9.16E-05
10	NM_052904	0.0025414	-4.57474	0.00020211
11	NM_001202550 /// NM_18	4.59E-05	-4.57483	0.000774529
12	NM_001199397 /// NM_00	0.00436131	-4.58074	0.00418935
13	NM_001268	0.0048873	-4.59453	0.034623
14	NM_139265	0.000122365	-4.5972	1.02E-05
15	NM_001079533 /// NM_00	2.18E-05	-4.59812	1.35E-07
16	NM_001003792 /// NM_00	0.00986927	-4.60167	0.000177592
17	NM_001012988 /// NR_02	0.00266927	-4.60399	0.0308087
18	NM_033058 /// NM_18408	0.0344661	-4.60482	0.000311009
19	NM_005634	0.00129238	-4.61092	2.17E-05
20	NM_004787	0.00217239	-4.61422	0.0141767
21	NM_144648	0.000618674	-4.61467	0.000836491
22	NM_013343 /// NR_02406	0.00562057	-4.62091	0.0031258
23	NM_001040113 /// NM_00	0.00106682	-4.62527	0.00314341
24	NM_001100590 /// NM_01	0.00234087	-4.62842	0.0121944
25	NM_001039704 /// NM_00	6.72E-05	-4.62889	3.47E-06
26	NM_020802	0.000807606	-4.6441	1.68E-05
27	NM_001135217 /// NM_00	0.00128545	-4.65049	0.000149798
28	NM_000081 /// NM_00100	0.00527437	-4.65752	0.00518535
29	NM_001145951 /// NM_00	0.000360419	-4.6587	0.00614451
30	NM_173354	0.0186595	-4.67151	0.00184981
31	NM_144992	0.000575529	-4.67589	2.60E-05
32	NM_001256295 /// NM_00	9.73E-05	-4.69101	2.87E-07
33	NM_025159	4.56E-06	-4.69767	0.000402758
34	NM_001153	0.000889361	-4.71763	0.0184164
35	---	2.20E-05	-4.7197	4.31E-07
36	NM_152290	0.000109205	-4.7258	9.34E-06
37	NM_001198625 /// NM_00	8.82E-05	-4.74991	2.06E-07
38	NM_001190458 /// NM_00	0.0023706	-4.75442	0.0138735
39	NM_001037763	0.00113925	-4.76204	0.00462377
40	NM_002228	0.00337577	-4.76249	0.0371813
41	NM_001243115 /// NM_02	1.86E-05	-4.76913	2.30E-05
42	NM_001077204 /// NM_02	0.00014263	-4.76966	0.00251606
43	NM_178827	5.04E-05	-4.77658	3.30E-05
44	NM_001202233 /// NM_00	0.00100318	-4.79102	0.00191128
45	NM_001013706	2.03E-06	-4.8072	5.32E-05
46	NM_001334	0.004717	-4.81126	0.000273768
47	NM_006633	0.000554563	-4.82025	0.00566488
48	NM_000476	0.0010715	-4.82172	7.47E-05

1	NM_014648	0.000732112	-4.82767	1.79E-05
2	NM_005112 /// NM_01749	0.000148107	-4.82951	0.00070615
3	NM_007050 /// NM_13317	0.000439522	-4.85087	0.00454172
4	NM_014549 /// NR_003714	0.00465514	-4.85284	0.0120334
5	NM_003462	0.024494	-4.85724	0.000691366
6	NM_025145	0.000922987	-4.85748	8.14E-05
7	NM_001001710	0.0013085	-4.8582	0.02541
8	NM_182628	0.00296713	-4.86484	0.000117209
9	NM_000348	4.72E-05	-4.88426	1.46E-05
10	NM_001198974 /// NM_20	0.000344635	-4.88696	0.00995334
11	NM_001114357	0.000311083	-4.88886	6.30E-06
12	NM_004120	0.000165584	-4.90185	0.000179444
13	NM_001122842 /// NM_00	0.00055417	-4.90764	9.56E-06
14	NM_002532	0.000507381	-4.91971	0.00110595
15	NM_001130046 /// NM_00	0.0120346	-4.91989	0.010802
16	NM_017439	0.00255228	-4.94463	0.00269797
17	NM_001127364 /// NM_00	0.000820982	-4.954	0.000315707
18	NM_002229	0.000202334	-4.96489	0.000139706
19	NM_000814 /// NM_00119	9.00E-05	-4.96628	1.01E-05
20	NM_173500	0.0019169	-4.97612	0.000173886
21	NM_015653	0.00889078	-4.97825	0.00180413
22	NM_145911	0.000154028	-4.98241	5.24E-05
23	NR_002798	0.000115006	-4.98982	8.81E-05
24	NM_001025436 /// NM_02	8.07E-06	-5.0083	9.55E-07
25	NM_022128	0.0049274	-5.01675	0.0160084
26	NM_001199880 /// NM_00	0.0422614	-5.02108	5.07E-06
27	NM_001206	0.00975839	-5.02289	0.015092
28	NM_001130518 /// NM_01	0.002211	-5.03631	0.000803956
29	NM_015347	0.000267401	-5.03841	0.00023689
30	NM_001001344 /// NM_02	0.000150803	-5.03962	0.00621483
31	NM_005516	0.000303639	-5.04804	0.0117163
32	NM_001280 /// NR_023312	6.74E-06	-5.04806	9.14E-05
33	NM_001010940	1.98E-05	-5.04922	9.98E-07
34	NM_001079821 /// NM_00	0.00846959	-5.05743	0.0271229
35	NM_001039799 /// NR_044	2.12E-07	-5.07092	8.64E-09
36	NM_144980	0.00117917	-5.08544	1.55E-06
37	NM_144975	2.39E-07	-5.09334	8.68E-05
38	NM_001029996	3.83E-05	-5.09559	0.000166108
39	NM_001033719	0.00552869	-5.10441	0.0217027
40	NM_001198625 /// NM_00	0.00108644	-5.10812	0.000776271
41	NM_001115	0.00363074	-5.12638	0.0129293
42	NM_001253854 /// NM_00	0.000462172	-5.1353	4.55E-05
43	NM_021784 /// NM_15367	0.000507499	-5.14251	3.68E-06
44	NM_033049	2.54E-06	-5.14593	2.14E-07
45	NM_000518	0.00464053	-5.14989	0.00501718
46	NM_021244	0.00778591	-5.15983	0.000601234
47	XR_110029 /// XR_133336	0.000509785	-5.1691	7.56E-05

1	NM_001143943 /// NM_03	0.010877	-5.20251	0.00283349
2	NM_001170538 /// NM_17	0.000608971	-5.20443	5.86E-06
3	NM_001111298 /// NM_17	0.0035917	-5.20746	0.000425257
4	NM_001242463 /// NM_05	0.0190955	-5.20912	0.00818638
5	NM_001025158 /// NM_00	4.89E-05	-5.23791	0.000252727
6	NM_001135608 /// NM_01	6.39E-05	-5.23951	0.00289677
7	NM_020643	1.45E-05	-5.24222	6.85E-05
8	NM_001190981 /// NM_00	7.89E-05	-5.24358	2.02E-06
9	NM_014331	0.00950634	-5.24409	0.000565266
10	NM_014312	0.000267384	-5.24596	0.00120336
11	NM_198493	0.000984614	-5.25696	0.000210136
12	NM_001004303	7.30E-06	-5.26	2.12E-06
13	NM_001105248 /// NM_00	0.000756173	-5.27187	0.000173885
14	NM_024764	0.000622845	-5.29344	0.0191701
15	NR_027105 /// NR_027106	0.007466	-5.30078	0.00106454
16	NM_001243848 /// NM_00	0.0046195	-5.30562	0.00524105
17	NM_001136020 /// NM_00	5.77E-09	-5.31628	6.52E-08
18	NM_001014986 /// NM_00	0.00156039	-5.32451	0.0056952
19	NM_001165963 /// NM_00	0.00260785	-5.33904	0.000446094
20	NR_004428	0.00722085	-5.34236	0.0302119
21	NM_025059	0.000620275	-5.34311	0.000750364
22	NM_001145313 /// NM_03	0.000428908	-5.34432	1.14E-05
23	NM_003853	0.00143847	-5.34758	0.00586326
24	XM_003403521 /// XM_00	0.00104659	-5.35234	0.000181694
25	NM_001134285 /// NM_00	0.000588726	-5.35616	0.0017975
26	NM_006408	0.000647935	-5.35983	2.25E-05
27	NM_018430	0.0003474	-5.38496	0.00058328
28	NR_003003	0.00232105	-5.40097	0.024489
29	NM_145020	0.000360031	-5.40987	1.30E-05
30	NM_004914	1.42E-07	-5.42467	1.54E-06
31	NM_015689	0.000118019	-5.42731	0.000118217
32	NM_006144	0.000265617	-5.43601	0.000325809
33	NM_001008539 /// NM_00	0.00140742	-5.43948	1.51E-08
34	NM_001102406 /// NM_00	6.51E-05	-5.44016	8.71E-05
35	NM_001134486 /// NM_05	0.00442711	-5.44263	0.0380487
36	NM_005013	0.0308436	-5.45252	0.0232975
37	NM_001130067 /// NM_01	0.00174365	-5.4671	0.000462761
38	NR_002174 /// NR_027626	0.000859072	-5.47354	0.000802378
39	NM_130446	1.26E-05	-5.47552	1.82E-05
40	NM_001098504 /// NM_00	0.00657283	-5.47675	0.00519342
41	NM_001099691 /// NM_00	0.00280448	-5.48538	0.00193834
42	NM_001040428 /// NM_01	0.00621799	-5.49527	0.0225875
43	NM_001099267 /// NM_00	0.000132947	-5.50108	5.50E-05
44	NM_006162 /// NM_17238	0.000246279	-5.51283	0.00794414
45	NM_020546	0.00184036	-5.51734	0.000141189
46	NM_001130182 /// NM_00	0.00291859	-5.51875	2.22E-05
47	NM_001280 /// NR_02331	1.69E-06	-5.5251	8.59E-06

1	NM_001243961 /// NM_00	0.00581218	-5.52644	0.00417962
2	NM_000246	6.90E-05	-5.53138	0.00277493
3	NM_001263	8.64E-05	-5.54058	0.000719274
4	NM_001161725 /// NM_00	0.000959167	-5.54285	0.00708675
5	NM_198520 /// XM_00171	0.00200182	-5.5431	2.64E-05
6	NM_001199805 /// NM_00	2.30E-06	-5.54685	0.000346706
7	NM_000301 /// NM_00116	0.000764418	-5.5663	2.68E-05
8	NM_018168	0.00257563	-5.59001	6.91E-08
9	NM_000814 /// NM_00119	0.000870233	-5.59069	6.32E-05
10	NM_000081 /// NM_00100	1.18E-05	-5.59524	0.000633885
11	NM_001001551 /// NM_00	0.00040087	-5.60619	0.00413702
12	NM_001102406 /// NM_00	3.18E-06	-5.61726	0.000169273
13	NM_001098515 /// NM_14	3.17E-06	-5.61828	0.00081076
14	NM_001178096 /// NM_00	0.00238816	-5.62334	0.000464495
15	NM_003012	0.000296682	-5.65041	1.19E-06
16	NM_001145399 /// NM_00	0.00294964	-5.65437	0.0418079
17	NM_005577	0.00418844	-5.67634	0.000452798
18	NM_003182 /// NM_01399	0.0185549	-5.69232	0.00319295
19	NM_054114 /// NM_13881	0.000692604	-5.70746	0.000805627
20	NM_003777	7.94E-07	-5.74836	8.94E-07
21	NM_001195415 /// NM_00	0.000649966	-5.75752	0.000582025
22	NM_001003799 /// NM_00	1.39E-05	-5.76143	1.51E-05
23	NM_001130831 /// NM_00	0.000228565	-5.76764	6.26E-05
24	NR_046102 /// XM_933872	0.00189241	-5.79165	0.000505536
25	NM_000933 /// NM_00117	0.00453076	-5.79639	0.00536709
26	NM_017590	0.000123797	-5.80309	0.00803712
27	NM_000720 /// NM_00112	6.01E-06	-5.83835	0.000104439
28	NM_002753 /// NM_13898	2.81E-05	-5.84239	6.78E-06
29	NM_021244	0.0282378	-5.84291	0.00140781
30	NM_145756	0.000265617	-5.84894	0.000725707
31	NM_174921	0.000139978	-5.87923	0.00213052
32	NM_001104629 /// NM_01	1.81E-05	-5.88792	0.000112717
33	NM_007116 /// NM_01910	0.000200396	-5.9039	4.12E-05
34	NM_178821	0.000777094	-5.92402	4.37E-05
35	NM_004155	4.11E-06	-5.9273	1.73E-06
36	NM_004529	0.000131277	-5.93034	1.57E-05
37	NM_153236	6.76E-06	-5.93344	1.11E-05
38	NM_001243961 /// NM_00	5.13E-06	-5.95048	1.55E-05
39	NM_001009991 /// NM_00	0.000284387	-5.95843	0.00041191
40	NM_004928	9.49E-07	-5.97752	0.000538943
41	NM_001223 /// NM_00125	1.14E-06	-5.99441	3.70E-05
42	NM_001159322 /// NM_00	8.18E-06	-5.99645	1.01E-05
43	NM_152772	0.00105898	-6.00294	0.00483128
44	NM_002984	1.07E-05	-6.01306	1.63E-05
45	NM_001001870 /// NM_03	2.01E-05	-6.02452	9.27E-07
46	NM_001198559 /// NM_01	3.46E-06	-6.04212	0.000241786
47	NM_007018	0.000115872	-6.04292	7.43E-06

1	NM_001190201 /// NM_00	7.73E-07	-6.05325	6.05E-07
2	NM_001242466 /// NM_18	0.00176049	-6.05958	0.0259266
3	NM_001162995 /// NR_01	6.59E-07	-6.07166	2.06E-05
4	NM_001031715 /// NM_02	0.00166765	-6.07213	4.36E-05
5	NM_023067	0.00283258	-6.07928	0.0301919
6	NM_021179	0.0111343	-6.08819	5.13E-05
7	NM_002970 /// NR_02778	3.34E-07	-6.09032	5.50E-06
8	NM_172069	0.00382923	-6.09141	0.000833211
9	NM_000636 /// NM_00102	0.0123088	-6.09667	0.00457304
10	NM_002864	2.51E-05	-6.10775	1.25E-05
11	NM_001002294 /// NM_00	4.78E-06	-6.11156	1.04E-06
12	NM_001204087 /// NM_00	4.56E-06	-6.11375	0.00215298
13	NM_005195	0.000262881	-6.13322	0.0013861
14	NM_001243280 /// NM_00	0.0192131	-6.13397	0.0289767
15	NM_004975	0.000981399	-6.15255	0.0321825
16	NM_000087 /// NM_00114	3.64E-06	-6.159	2.29E-05
17	NM_021101	0.00227907	-6.16281	0.00035475
18	NM_001078 /// NM_00119	0.0220099	-6.16839	0.000906967
19	NM_003619	0.00201383	-6.16977	3.41E-05
20	NM_002259 /// NM_00226	4.91E-05	-6.19084	1.25E-06
21	NM_152643	3.32E-07	-6.20708	3.47E-07
22	NM_004420	3.60E-05	-6.22377	0.00363493
23	NM_001142462 /// NM_05	0.0109399	-6.27368	0.0028817
24	NR_001564	0.0103542	-6.30367	0.00125762
25	NM_001040280 /// NM_00	0.00026411	-6.3039	7.32E-06
26	NM_001267048 /// NM_00	0.0212537	-6.3162	0.0483302
27	NM_178527	0.000183459	-6.31871	6.15E-06
28	NM_001756	3.89E-05	-6.32156	2.31E-05
29	NM_000892	0.000247453	-6.33372	0.000557259
30	NM_013262	0.000805201	-6.34818	0.0221915
31	NM_015675	0.000977817	-6.34899	0.00981342
32	NM_001031745 /// NM_00	4.72E-05	-6.35907	1.71E-05
33	NM_022785 /// NM_19885	3.71E-05	-6.37722	9.03E-06
34	NM_145047 /// NM_20683	0.000916127	-6.38992	0.0225337
35	NM_030666	6.69E-08	-6.39749	7.94E-07
36	NM_001014986 /// NM_00	0.000227376	-6.39986	0.00439886
37	NM_001242350 /// NM_00	1.67E-07	-6.40309	1.62E-07
38	NR_002819 /// XR_110915	0.000145618	-6.40314	0.0172489
39	NM_152701	0.000587293	-6.4179	1.75E-05
40	NM_000609 /// NM_00103	0.00126344	-6.43135	4.49E-05
41	NM_001099267 /// NM_00	1.86E-05	-6.45461	1.57E-07
42	NM_144992	0.000180517	-6.47126	2.51E-05
43	NM_007037	5.85E-07	-6.48673	9.17E-06
44	NM_000856 /// NM_00113	0.000276251	-6.51278	9.86E-06
45	NM_005618	0.00281377	-6.53253	0.0114133
46	NM_002581	0.00248966	-6.53397	0.000437903
47	NM_018076	0.00348075	-6.53445	8.16E-06

1	NM_001127608 /// NM_00	5.81E-06	-6.5351	0.00213401
2	NM_014395	2.12E-09	-6.53973	4.62E-06
3	NM_001270391 /// NM_00	1.15E-05	-6.54251	1.32E-07
4	NM_003320 /// NM_17797	0.000509948	-6.54857	0.0117307
5	NM_031490 /// NR_04067	1.73E-06	-6.55714	0.000204493
6	NM_001033659 /// NM_00	0.00152329	-6.56694	0.0186456
7	NM_001122769 /// NM_18	0.000556567	-6.56912	0.00105189
8	NM_001243797 /// NM_00	0.000409307	-6.59297	0.000555192
9	NM_174896	2.25E-05	-6.61814	0.00718602
10	NM_001164407	0.00107983	-6.62037	0.00282217
11	NM_001242524 /// NM_00	7.99E-05	-6.62074	6.01E-05
12	NM_001256552 /// NM_02	1.16E-07	-6.63141	4.48E-05
13	NM_001206609 /// NM_00	5.50E-08	-6.63783	4.02E-06
14	NM_017539	0.000199545	-6.66492	4.70E-05
15	NM_001253835 /// NM_00	5.66E-05	-6.68502	0.000198292
16	NM_002937 /// NM_19443	3.31E-05	-6.6881	0.000291652
17	NM_001130715 /// NM_00	0.00133595	-6.74603	2.10E-06
18	NM_007116 /// NM_01910	3.15E-05	-6.75806	8.18E-05
19	NM_006955	3.55E-06	-6.7602	0.000508887
20	NM_012307	0.000445881	-6.7709	9.49E-05
21	NM_152377	6.55E-05	-6.77116	6.20E-07
22	NM_014203 /// NM_13078	0.000343588	-6.78374	0.0064001
23	NM_145172	0.00145927	-6.78542	9.11E-06
24	NM_001130918 /// NM_17	2.05E-05	-6.82071	2.71E-06
25	NM_001164342 /// NM_00	6.25E-05	-6.83161	0.0141681
26	NM_001122824 /// NM_00	0.000166787	-6.83438	3.89E-05
27	NM_052863	0.00181971	-6.84023	0.0160659
28	NM_001184879 /// NM_00	2.45E-05	-6.85153	0.00306037
29	NM_000313	0.0076936	-6.85305	0.0336922
30	NM_001031741 /// NM_15	1.02E-05	-6.85413	1.58E-05
31	NM_152271	1.61E-05	-6.85792	8.10E-05
32	NM_001010848 /// NM_00	0.000352596	-6.8723	0.000143549
33	NM_001099267 /// NM_00	0.000511873	-6.89266	8.14E-08
34	NM_002581	0.0254171	-6.89681	0.00493725
35	NM_003948	0.00106683	-6.90512	0.0157673
36	NM_001004416 /// NM_00	0.000464768	-6.91989	0.000115634
37	NM_001034850 /// NM_01	0.00175417	-6.93	0.0032106
38	NM_001144382 /// NM_01	0.000645371	-6.93481	0.000146518
39	NM_001256295 /// NM_00	3.19E-07	-6.94979	2.50E-07
40	NM_033124	0.000137115	-6.95492	3.32E-05
41	NM_000218 /// NM_18179	1.38E-08	-6.97664	8.23E-05
42	NM_001168374 /// NM_00	9.86E-06	-6.9949	6.17E-07
43	NM_001122834 /// NM_00	2.31E-05	-7.00114	0.000281356
44	NR_038311 /// NR_038312	0.000120721	-7.00528	0.00813951
45	NM_145740	2.84E-05	-7.03298	7.27E-05
46	NM_001029875	1.00E-06	-7.03534	8.10E-08
47	NM_001243848 /// NM_00	0.00454913	-7.04702	0.00657549

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2	NM_013367	0.000290644	-7.04819	0.0014394
3	NM_007116 /// NM_01910	2.69E-05	-7.05831	8.62E-05
4	NM_001220765 /// NM_00	0.002131	-7.07456	0.0300976
5	NM_003734	0.000298491	-7.09585	0.0222615
6	NM_001077416 /// NM_00	0.000336895	-7.11867	8.57E-06
7	NM_015417	9.18E-05	-7.12947	0.000816937
8	NM_153274	0.0017085	-7.18313	0.00783475
9	NM_022570 /// NM_19794	5.97E-06	-7.19153	0.000857727
10	NM_012472	0.000519042	-7.19335	0.0171137
11	NM_001197295 /// NM_00	0.000322244	-7.19564	0.00286542
12	NM_000044 /// NM_00101	0.000100589	-7.20021	0.00351045
13	NM_002985	9.67E-06	-7.21984	0.000821151
14	NM_001039706 /// NM_00	6.91E-05	-7.24371	7.68E-05
15	NM_003246	0.000703866	-7.2513	0.0037798
16	NM_015202	1.96E-06	-7.28771	0.000130899
17	NM_001039948 /// NM_00	8.11E-06	-7.29193	3.45E-06
18	NM_004058 /// NM_08059	0.0116539	-7.30487	0.00767003
19	NM_005847 /// NM_15268	0.00143407	-7.3218	0.0023194
20	NR_001298	1.93E-05	-7.35774	0.000227348
21	NM_001009991 /// NM_00	3.50E-08	-7.37057	1.54E-05
22	NM_004288	0.000304692	-7.40166	0.00830185
23	NM_002919 /// NM_13442	0.00236768	-7.40225	0.00114519
24	NM_000635 /// NM_13443	0.000829277	-7.40233	1.55E-05
25	NM_001199739 /// NM_00	4.28E-06	-7.41416	2.30E-06
26	NM_198282	1.32E-05	-7.41975	2.81E-05
27	NM_016270	1.44E-05	-7.42316	1.58E-05
28	NM_001201466 /// NM_03	2.94E-06	-7.42559	1.21E-06
29	NM_005727	0.00123627	-7.43629	0.0105965
30	NM_017699	5.05E-06	-7.43751	4.60E-08
31	NM_001039706 /// NM_00	2.71E-05	-7.4469	0.00185413
32	NM_018222	1.15E-06	-7.45192	0.000125391
33	NM_002985	7.44E-05	-7.46459	0.00147074
34	NM_018897	2.22E-06	-7.46587	1.42E-06
35	NM_001370 /// NM_17364	0.000211815	-7.46769	1.34E-05
36	NM_001025076 /// NM_00	0.000353146	-7.46918	0.000221836
37	NM_000720 /// NM_00112	7.45E-05	-7.5016	0.00163536
38	NM_006408	0.00326004	-7.51037	7.37E-08
39	NM_058180 /// NM_19907	0.00176094	-7.51893	0.00583408
40	NM_001161661 /// NM_00	0.000196344	-7.52512	0.00905524
41	NM_001134649 /// NM_00	0.00198616	-7.54862	0.0282364
42	NM_001001437 /// NM_00	0.000679056	-7.55377	0.000747315
43	NM_130446	2.45E-06	-7.55487	1.35E-05
44	NM_000855 /// NM_00125	0.000451399	-7.5579	5.58E-05
45	NM_001134363	0.000636723	-7.55977	3.58E-05
46	XR_040780	1.30E-05	-7.57129	7.24E-06
47	NM_144702	3.98E-06	-7.5832	1.30E-07
48	NM_000833 /// NM_00113	0.00252652	-7.5878	0.0386345
49				
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52				
53				
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57				
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1	NM_001470 /// NM_00639	0.00564045	-7.6113	0.0438321
2	NM_001460	0.016143	-7.63329	0.0394321
3	NM_000847	1.57E-06	-7.63426	2.13E-07
4	NM_030906	0.000205467	-7.67853	2.82E-06
5	NM_001025081 /// NM_00	0.000822197	-7.68541	0.00420404
6	NM_015512	5.00E-05	-7.69301	0.000982024
7	NM_025057	0.00101255	-7.69324	0.000951393
8	NM_001039936 /// NM_00	0.00117187	-7.69936	0.000736467
9	NM_014395	8.45E-06	-7.71739	0.000201919
10	NM_012337	0.0015375	-7.73044	2.62E-05
11	NM_013308	0.000832605	-7.73066	0.00141214
12	NM_001145365 /// NM_01	0.000715293	-7.76748	0.0336268
13	NM_145045	0.000176067	-7.77734	0.0298979
14	NM_001920 /// NM_13350	0.00131874	-7.81523	0.00882708
15	NM_002185	0.000109863	-7.82528	5.75E-06
16	NM_001270391 /// NM_00	1.22E-06	-7.84599	3.01E-07
17	NM_014861	4.22E-06	-7.85372	9.88E-06
18	NM_001199633 /// NM_02	3.25E-05	-7.85924	7.40E-05
19	NM_004751	5.40E-06	-7.88014	4.36E-05
20	NM_001267048 /// NM_00	0.00797869	-7.88468	0.0174149
21	NM_020957	0.0003204	-7.89211	0.0311343
22	NM_153267	9.40E-05	-7.90797	6.19E-06
23	NM_006063	0.000885156	-7.98559	0.0107881
24	NM_001127603 /// NM_01	6.55E-05	-7.99949	0.0196598
25	NM_024753 /// NR_04537 ^t	2.83E-05	-8.00715	8.76E-05
26	NM_021201 /// NM_20693	0.000392632	-8.01056	0.0102077
27	NM_002119	2.26E-05	-8.01237	0.000152428
28	NM_003059	0.000346655	-8.05806	2.62E-06
29	NM_022785 /// NM_19885	0.000135295	-8.10895	1.17E-05
30	NM_001037500	1.35E-05	-8.12989	6.49E-05
31	NM_001128432 /// NM_02	0.00077688	-8.1565	0.000240739
32	NM_001206	0.000249108	-8.15894	0.0106346
33	NM_001098519 /// NM_15	4.28E-05	-8.17174	3.18E-06
34	NM_001146192 /// NM_03	0.000595417	-8.19358	0.00104437
35	NM_001243280 /// NM_00	0.00694336	-8.19971	0.00896409
36	NM_001080467	5.40E-07	-8.20601	6.99E-05
37	NM_182500	8.08E-05	-8.20878	1.29E-05
38	NM_001099697 /// NM_17	7.30E-06	-8.22423	8.47E-07
39	NM_001040429 /// NM_01	0.000805889	-8.22896	0.00881614
40	NM_012435	1.77E-06	-8.25637	4.60E-05
41	NM_014861	8.12E-09	-8.26039	1.26E-07
42	NM_033063 /// NM_20757	1.47E-06	-8.27802	8.32E-08
43	NM_001256054 /// NM_01	0.00351451	-8.27995	0.00129025
44	NM_001085	0.00426915	-8.28422	1.12E-05
45	NM_014935 /// NM_13848	3.76E-05	-8.28598	0.00326299
46	NM_001031802 /// NM_00	1.84E-05	-8.28676	7.31E-05
47	NM_018399 /// NM_07862	9.62E-05	-8.3271	1.41E-06

1				
2	NM_017600 /// NR_02426:	4.63E-05	-8.34882	0.00284749
3	NM_001267576 /// NM_15	0.000139566	-8.35442	0.000211626
4	NM_002581	7.41E-06	-8.38336	2.18E-05
5	NM_001193434 /// NM_00	0.00393152	-8.38953	0.048983
6	NM_002970 /// NR_02778:	2.06E-08	-8.42189	7.38E-07
7	NM_000715	1.95E-05	-8.43361	3.10E-05
8	NM_138801	7.54E-06	-8.43611	0.00114876
9	NM_002612	0.00121036	-8.45886	4.16E-06
10	NM_001172684 /// NM_00	3.10E-06	-8.46072	0.00133203
11	NM_000219 /// NM_00112	0.000988214	-8.46388	0.000112171
12	NR_015377 /// NR_047570	2.10E-05	-8.51364	0.000221521
13	NR_034012 /// NR_034013	0.000180003	-8.52589	4.70E-06
14	NM_001193489 /// NM_01	3.25E-05	-8.53102	0.00774004
15	NM_138409	0.00639711	-8.62206	0.002328
16	NM_001165 /// NM_18296	0.000172485	-8.63478	3.27E-06
17	XR_109454 /// XR_111677	0.00518014	-8.64842	0.000482511
18	NM_000591 /// NM_00104	0.000334983	-8.65813	0.0136641
19	NM_138451	0.000444867	-8.67529	0.00223138
20	NM_001039395 /// NM_01	1.74E-06	-8.68129	1.11E-07
21	NM_001130699 /// NM_00	4.05E-05	-8.75233	0.0173095
22	NM_138444	0.00175791	-8.78668	0.00144355
23	NM_006290	5.71E-05	-8.80832	0.00040811
24	NM_001204458 /// NM_00	0.00143956	-8.83669	0.0226359
25	NM_001040113 /// NM_00	3.73E-06	-8.83787	0.000199129
26	NM_025087	0.000694501	-8.84041	1.34E-05
27	NM_017886	3.93E-05	-8.85287	0.00154039
28	NM_000565 /// NM_00120	0.000164036	-8.8565	0.0114806
29	NM_001554	0.00099024	-8.85749	0.00494922
30	NM_001164342 /// NM_00	7.50E-05	-8.87015	0.00772664
31	NM_015693	0.00181615	-8.88234	0.000199537
32	NM_015896	0.00145148	-8.92236	0.000119364
33	NM_001112717 /// NM_00	0.000439766	-8.93603	0.014312
34	NM_014211	0.00423217	-8.93771	0.0306518
35	NM_001012642	8.34E-05	-8.94894	0.018175
36	NM_000104	1.33E-06	-8.95504	3.44E-05
37	NM_001136536 /// NM_00	6.84E-05	-8.97068	1.65E-06
38	NM_001039845 /// NM_20	5.50E-06	-8.99984	2.64E-05
39	NM_004310	7.51E-05	-9.02095	0.000302279
40	XR_109365 /// XR_111668	6.80E-06	-9.03992	6.01E-05
41	NM_001247997 /// NM_00	8.60E-06	-9.05639	0.00377279
42	NM_001114106 /// NM_00	5.13E-05	-9.13421	0.000109188
43	NM_002221	0.000234046	-9.13645	0.0235181
44	NM_001037290 /// NM_00	0.000178028	-9.14721	0.00029647
45	NM_000480 /// NM_00102	5.14E-05	-9.14962	0.000107298
46	NM_020225	4.32E-08	-9.15903	0.000731081
47	NM_001118 /// NM_00119	0.000693518	-9.26258	0.000263657
48	NR_027046	6.68E-08	-9.29354	0.000238534

1	NM_001164257 /// NM_00	1.44E-07	-9.30234	8.37E-08
2	NM_025153	0.000198798	-9.30373	0.00051513
3	NM_001242505 /// NM_00	0.00880551	-9.32858	0.0448283
4	NM_001171171 /// NM_00	0.00151631	-9.39197	0.0126955
5	NM_003672 /// NM_03331	0.000255109	-9.39641	0.000150809
6	NM_000672 /// NM_00110	0.000438064	-9.40483	1.66E-05
7	NM_001080529	3.11E-05	-9.41658	0.000249196
8	NM_001031743 /// NM_17	2.59E-05	-9.41901	2.78E-05
9	NR_002819 /// XR_110915	5.07E-07	-9.42774	0.00237192
10	NM_001005474 /// NM_03	2.13E-06	-9.44188	1.07E-07
11	NM_001099410 /// NM_00	1.15E-05	-9.44342	0.00280929
12	NM_001143943 /// NM_03	0.000702769	-9.46255	0.00136054
13	NM_032411	0.00529664	-9.46871	0.0316644
14	NM_001280 /// NR_02331	9.24E-08	-9.51331	3.05E-05
15	NM_024786	1.74E-06	-9.52737	0.00340169
16	NM_152376	5.83E-06	-9.53705	3.29E-06
17	NM_017600 /// NR_02426	2.49E-07	-9.5394	0.000454747
18	NM_001145811 /// NM_00	1.41E-06	-9.56269	0.00109777
19	XR_108456	0.000781956	-9.56919	0.0091861
20	NM_175922	0.000176543	-9.60043	1.09E-05
21	NR_038877	0.000919218	-9.62902	0.00217758
22	NM_152376	0.000450347	-9.64026	4.64E-05
23	NM_001136105	0.000820202	-9.64704	7.37E-05
24	NM_000130	6.40E-05	-9.68778	1.77E-06
25	NM_004585	4.87E-05	-9.70238	0.00108961
26	NM_000348	0.000234138	-9.70691	5.39E-06
27	NR_040109	0.000427623	-9.71612	1.91E-05
28	NM_003672 /// NM_03331	2.82E-05	-9.78083	0.000812194
29	NM_005045 /// NM_17305	8.79E-05	-9.78253	0.0128318
30	NM_001171581 /// NM_00	0.000137834	-9.80861	6.39E-05
31	NM_001134285 /// NM_00	0.00207945	-9.82216	0.00613468
32	NM_001040429 /// NM_01	0.0024324	-9.85095	0.00590646
33	NM_000961	7.19E-05	-9.89193	0.00560389
34	XR_109227 /// XR_133091	0.000224925	-9.8948	0.0170891
35	NM_002118	6.60E-05	-9.93181	0.0124423
36	NM_001164730 /// NM_00	7.85E-05	-9.93633	1.79E-05
37	NM_001005474 /// NM_03	3.83E-06	-9.94885	4.53E-07
38	NM_001223 /// NM_00125	1.16E-05	-9.96	0.000414357
39	NM_024865	2.99E-05	-9.98179	0.00301072
40	NM_001244134 /// NM_00	1.57E-06	-9.99812	0.000109954
41	NM_000399 /// NM_00113	0.00141731	-10.074	0.00246235
42	NM_145038	5.51E-06	-10.151	1.63E-05
43	NM_024081	0.000338222	-10.1686	0.0103363
44	NM_001370 /// NM_17364	0.000104261	-10.2019	8.71E-06
45	NM_001007267 /// NM_00	0.0003687	-10.2544	0.0151942
46	NM_000517 /// NM_00055	0.007001	-10.3106	0.00740361
47	NM_152505	1.01E-06	-10.3119	4.92E-08

1	NM_006120	4.08E-05	-10.3903	0.000390878
2	NM_001006655 /// NM_01	0.000221993	-10.4572	3.60E-05
3	NM_032131	0.000124519	-10.462	1.40E-05
4	NM_001034850 /// NM_01	4.71E-06	-10.4718	6.02E-05
5	NM_005565	2.92E-06	-10.4786	6.91E-06
6	NM_001002294 /// NM_00	6.74E-05	-10.4903	7.79E-06
7	NM_001080394 /// XM_00	5.12E-06	-10.4914	2.09E-05
8	NM_002581	0.000157011	-10.5359	0.000149268
9	NM_001100388 /// NM_20	3.09E-05	-10.612	4.35E-07
10	NM_014496	0.000225821	-10.6347	0.00432471
11	NM_031412 /// NR_02828	3.27E-07	-10.6496	0.00194191
12	NM_001145646 /// NM_03	5.25E-07	-10.7244	1.20E-05
13	NM_001025076 /// NM_00	1.06E-07	-10.7515	4.41E-05
14	NM_175709	1.95E-07	-10.7539	0.000145516
15	NM_001039763	2.30E-07	-10.7767	5.79E-09
16	XR_133404	2.77E-05	-10.8158	4.78E-06
17	NM_001243342 /// NM_01	3.77E-08	-10.8514	2.53E-08
18	NM_001089584	4.19E-05	-10.8864	3.80E-06
19	NM_030906	6.18E-05	-10.9275	3.25E-06
20	NM_001242463 /// NM_05	3.47E-05	-10.9832	0.00180351
21	NM_001270391 /// NM_00	0.000201336	-10.9923	3.69E-06
22	NM_001037582 /// NM_02	9.38E-06	-10.9976	0.000753929
23	NM_006206	0.000316829	-11.0029	0.000159065
24	NM_173605 /// NM_19946	0.000114696	-11.0742	1.27E-06
25	NM_014265 /// NM_02177	0.000563749	-11.0877	0.00108208
26	NM_001172420 /// NM_01	7.40E-07	-11.1177	1.82E-06
27	NM_001006655 /// NM_01	1.98E-05	-11.1543	2.85E-06
28	NR_037901	3.88E-05	-11.2077	3.38E-06
29	NM_001122961	1.81E-05	-11.2118	1.34E-06
30	NM_001037763	0.000166335	-11.2275	1.44E-05
31	NM_080283 /// NM_17238	0.000240286	-11.2428	0.000213834
32	NM_001206997 /// NM_15	3.28E-05	-11.2519	2.20E-07
33	NM_002970 /// NR_02778	3.03E-10	-11.2949	9.14E-06
34	NM_001007278 /// NM_00	0.000151368	-11.3411	1.60E-06
35	NM_024763 /// NM_20701	8.88E-06	-11.4101	2.64E-05
36	NM_001167942 /// NM_15	0.000100698	-11.4266	6.92E-05
37	NM_178818 /// NM_18152	2.67E-07	-11.4758	0.0027691
38	NM_007030	3.45E-05	-11.4966	0.000530138
39	NM_001080529	1.33E-07	-11.5519	1.98E-07
40	NM_001204197 /// NM_01	2.48E-07	-11.5545	1.49E-08
41	NM_001042519 /// NM_00	0.000667317	-11.574	0.0224574
42	NM_000565 /// NM_00120	0.000198459	-11.6062	0.00512886
43	NM_001256113 /// NM_17	6.00E-06	-11.6104	2.13E-05
44	NM_001039350 /// NM_00	0.000297046	-11.6224	0.000222651
45	NM_001201466 /// NM_03	0.00160949	-11.6789	0.000647665
46	NM_000855 /// NM_00125	0.000170077	-11.6881	3.98E-05
47	NM_001001706 /// NM_00	2.87E-06	-11.7047	4.27E-07

1	NM_006981 /// NM_17319	0.000218591	-11.7215	0.000313792
2	NM_003986	0.000272156	-11.8011	0.00305906
3	NM_001142857 /// NM_02	4.66E-06	-11.8081	5.14E-08
4	NM_004058 /// NM_08059	5.56E-05	-11.8103	0.000109162
5	NM_001253908 /// NM_00	0.000290037	-11.8301	1.80E-05
6	NM_005746 /// NM_18279	8.39E-05	-11.8341	5.77E-07
7	NM_001010892 /// NM_00	0.000580144	-11.8722	1.51E-05
8	NM_001112706 /// NM_03	0.00014107	-11.8956	8.60E-06
9	NM_001199739 /// NM_00	4.05E-06	-11.9055	6.66E-06
10	NM_174912	4.08E-09	-11.9698	4.33E-05
11	NM_001083 /// NM_03343	4.29E-06	-12.0119	1.05E-06
12	NM_001144033 /// NM_14	0.00114305	-12.0417	4.90E-05
13	NM_024940	4.53E-05	-12.1164	0.000259729
14	NM_173615 /// NM_17505	5.99E-07	-12.1508	2.07E-07
15	NM_001669 /// NM_00958	4.26E-07	-12.1734	0.000836802
16	NM_012144	1.97E-06	-12.2254	1.31E-07
17	NM_018423	0.000208879	-12.2304	0.00981492
18	NM_001141945 /// NM_00	0.000358753	-12.2508	0.0209401
19	NM_001202233 /// NM_00	0.000131522	-12.257	0.00130173
20	NM_001242935 /// NM_00	2.85E-06	-12.2946	6.96E-05
21	NM_001781 /// NR_02667	2.46E-06	-12.3527	3.36E-09
22	NM_006235	0.000187704	-12.3623	4.97E-06
23	NM_001018046 /// NM_02	4.56E-05	-12.4587	2.51E-06
24	NM_001195303 /// NM_00	0.000191635	-12.515	0.00023016
25	NM_015351	1.09E-05	-12.582	0.00945982
26	NM_001190726 /// NM_03	1.30E-06	-12.6104	0.000567328
27	NM_001142857 /// NM_02	7.99E-06	-12.686	4.35E-07
28	NM_001003674 /// NM_00	9.39E-05	-12.6882	0.00711703
29	NM_001156474 /// NM_02	2.94E-07	-12.6941	8.64E-09
30	NM_198078 /// NR_02727	0.000404714	-12.7773	0.00145459
31	NM_007335 /// NM_00733	5.90E-06	-12.7967	2.96E-06
32	NM_001114094 /// NM_00	1.27E-05	-12.8215	0.010032
33	NM_001080850	9.68E-06	-12.8285	0.0107224
34	NM_001002233 /// NM_00	3.54E-05	-12.8451	0.00163819
35	NM_024574	2.34E-05	-12.9495	1.69E-05
36	NM_020893 /// NR_03652	3.31E-05	-13.0256	0.000984417
37	NM_001076778 /// NM_00	6.93E-06	-13.0296	0.00979652
38	NM_018429	4.91E-05	-13.0447	0.0267189
39	NM_001164496 /// NM_01	1.44E-05	-13.0974	8.53E-05
40	NM_001008723	6.40E-05	-13.0985	1.33E-06
41	NM_172193	0.0001053	-13.1863	0.00135122
42	NM_001243961 /// NM_00	0.0024713	-13.2167	0.00464605
43	NM_198282	2.39E-07	-13.2574	2.21E-05
44	NM_002847 /// NM_13084	3.26E-05	-13.3015	2.91E-05
45	NM_001144956	7.54E-05	-13.3067	1.15E-06
46	NM_001169154 /// NM_17	4.84E-05	-13.3092	1.70E-06
47	NM_001149 /// NM_00120	1.31E-06	-13.3434	0.013086

1				
2	NM_033364 /// XR_132494	0.000112205	-13.3626	0.00557221
3	NM_006186 /// NM_17317	3.15E-06	-13.3741	8.19E-06
4	NM_031898	9.23E-05	-13.3787	1.90E-06
5	NM_000720 /// NM_00112	2.15E-05	-13.3978	0.0031304
6	NM_001131010 /// NM_00	0.000372	-13.4158	7.69E-06
7	NM_025244 /// NM_18291	4.73E-05	-13.468	8.61E-06
8	NM_001029996	1.34E-05	-13.6013	1.50E-06
9	NM_001159629 /// NM_00	0.000725818	-13.638	3.13E-06
10	NM_000777 /// NM_00119	3.26E-05	-13.6676	0.00109274
11	NM_001267798 /// NM_00	2.82E-06	-13.7008	0.000263889
12	NM_001996 /// NM_00648	1.37E-06	-13.7281	6.11E-05
13	NM_001001971 /// NM_00	7.08E-05	-13.7371	1.93E-05
14	NM_139172	0.000576014	-13.8348	0.000451422
15	NM_002090	0.000304404	-13.852	4.51E-05
16	NM_001079691 /// NM_05	1.71E-07	-13.9109	6.59E-05
17	NM_001159643 /// NM_00	5.92E-08	-13.9194	2.65E-05
18	NM_001253854 /// NM_00	4.24E-05	-13.9721	1.72E-07
19	NM_001131010 /// NM_00	0.000246848	-14.0774	0.000113956
20	NM_025153	0.0016689	-14.0836	0.0193682
21	NM_001135919 /// NM_18	7.78E-07	-14.0897	0.000626824
22	NM_002727 /// NR_036430	0.000103262	-14.1337	0.00224487
23	NM_152327	2.13E-05	-14.1696	1.70E-05
24	NM_001008409	0.000175302	-14.1922	0.0100234
25	NR_002722 /// NR_024553	4.76E-06	-14.1924	8.63E-06
26	NM_001669 /// NM_00958	2.75E-05	-14.197	0.00047441
27	NM_016557 /// NM_17844	2.15E-06	-14.2585	5.86E-08
28	NM_006217	0.000294616	-14.2621	0.000376125
29	NM_001039763	0.000755146	-14.3132	1.86E-05
30	NM_001025158 /// NM_00	7.33E-07	-14.3951	2.56E-06
31	NM_018897	1.59E-05	-14.4463	2.13E-06
32	NM_001001523 /// NM_00	5.00E-07	-14.557	2.66E-05
33	NM_001270383 /// NM_14	4.39E-05	-14.6823	1.17E-05
34	NM_001045476	5.89E-06	-14.6842	4.06E-07
35	NM_016234 /// NM_20337	2.26E-08	-14.6873	1.41E-05
36	NM_001146003 /// NM_02	3.55E-08	-14.8307	0.000139559
37	NM_001076778 /// NM_00	1.60E-06	-14.907	0.00945191
38	NM_003890	0.000100009	-14.9479	0.0291036
39	NM_138468 /// NM_17823	1.69E-05	-14.9814	0.000360393
40	NM_000689	2.70E-07	-14.9966	2.80E-08
41	NM_182508	0.000766464	-15.0216	4.86E-05
42	NM_000963	5.38E-06	-15.0244	2.47E-09
43	NM_001159629 /// NM_00	6.70E-05	-15.1084	7.54E-08
44	NM_001145811 /// NM_00	2.98E-06	-15.1231	0.0112807
45	NM_001114357	0.000117511	-15.1455	5.85E-05
46	NM_004235	3.95E-05	-15.1767	7.05E-07
47	NM_020802	8.58E-05	-15.253	2.73E-06
48	NM_001164407	2.61E-05	-15.3543	0.0031387
49				
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1	NM_001669 /// NM_00958	5.42E-06	-15.4184	0.000525683
2	NM_006763	4.03E-05	-15.4279	0.000101711
3	NM_001256054 /// NM_01	3.02E-07	-15.4331	5.58E-07
4	NM_001146319 /// NM_00	6.65E-05	-15.4939	0.0433328
5	NM_015668	1.64E-05	-15.4969	4.29E-06
6	NM_001012502	1.14E-06	-15.5255	1.68E-07
7	NM_004616	0.000297612	-15.5514	0.0011123
8	NM_001105513 /// NM_14	7.58E-05	-15.6444	0.00943173
9	NM_152576 /// XR_108934	1.47E-05	-15.7815	0.00134501
10	NM_001039845 /// NM_20	2.91E-07	-15.8287	7.39E-05
11	NM_005832 /// NM_18136	0.000179821	-15.9058	7.01E-05
12	NM_032606	0.000124155	-15.9335	4.64E-07
13	NM_004417	1.08E-05	-15.9636	8.91E-06
14	NM_153228	3.00E-06	-16.0028	6.25E-08
15	NM_001199989 /// NM_01	4.86E-05	-16.0373	0.000120973
16	NM_001733	1.20E-07	-16.1295	0.00696591
17	NM_003551	3.07E-06	-16.1749	1.42E-06
18	NM_001001991 /// NM_01	3.12E-07	-16.2852	3.65E-06
19	NM_007335 /// NM_00733	6.27E-06	-16.2924	7.72E-07
20	NM_019111	1.79E-05	-16.2929	0.000945978
21	NM_001162371	0.000121315	-16.3053	0.00420868
22	NM_004666	4.42E-05	-16.3388	1.89E-07
23	NM_014057 /// NM_02441	0.000227999	-16.4164	7.12E-06
24	NM_001920 /// NM_13350	1.36E-05	-16.439	0.0118227
25	NM_001242385 /// NM_00	1.27E-07	-16.4699	9.21E-09
26	XR_133482	1.53E-05	-16.4744	2.82E-07
27	NM_000855 /// NM_00125	0.000129445	-16.5856	1.28E-05
28	NM_001098843	3.50E-05	-16.6306	5.26E-05
29	NM_001193341 /// NM_15	1.01E-06	-16.699	1.97E-07
30	NM_0000014	1.22E-05	-16.827	0.0373429
31	NM_001135934 /// NM_00	0.00842392	-16.8567	0.0049334
32	NM_019111	3.55E-06	-16.9104	6.41E-05
33	NM_002121	1.76E-05	-16.9362	0.000522919
34	NM_001198625 /// NM_00	0.000133635	-16.9711	6.81E-05
35	NM_031461	0.000529161	-16.9816	0.000575821
36	XR_110232 /// XR_111449	2.30E-05	-16.9955	1.08E-06
37	NM_001430 /// XR_132707	8.36E-06	-17.1061	0.00609928
38	NM_001128602 /// NM_00	5.64E-05	-17.1151	0.00085383
39	NM_144676	2.09E-05	-17.1536	8.62E-08
40	NM_024786	2.99E-05	-17.2701	0.00575643
41	NM_014365	1.35E-06	-17.3629	1.67E-06
42	NM_001669 /// NM_00958	2.06E-06	-17.3701	0.000614037
43	NM_000700	0.000633163	-17.518	0.00453511
44	NM_152784	2.01E-06	-17.5509	1.05E-08
45	NM_000104	1.10E-05	-17.5993	0.000564276
46	NM_020734	1.97E-05	-17.6179	0.0427005
47	NM_014859	1.18E-06	-17.6611	1.65E-05

1				
2	NM_000416	3.16E-06	-17.7704	0.000881786
3	NM_020802	6.89E-10	-17.8037	5.96E-12
4	NM_053285	0.000143758	-17.9309	2.58E-06
5	NM_002122 /// NM_02005	0.000281988	-17.9649	0.000211915
6	NM_000898	1.16E-05	-18.097	3.17E-05
7	NM_006186 /// NM_17317	0.000100252	-18.154	8.39E-05
8	NM_000278 /// NM_00398	0.00171176	-18.1782	0.00429549
9	NM_001243961 /// NM_00	7.68E-05	-18.1797	0.000469985
10	NM_017424 /// NM_17740	7.25E-08	-18.1844	8.40E-05
11	NM_001033658 /// NM_00	6.36E-05	-18.2079	0.000164184
12	NM_001205288 /// NM_03	0.00013309	-18.4945	0.0347131
13	NM_058186 /// NM_20696	2.48E-05	-18.5145	0.00136155
14	NM_001178003 /// NM_14	6.53E-05	-18.5595	7.09E-06
15	NM_001159643 /// NM_00	2.38E-05	-18.6732	0.000159714
16	NM_001164496 /// NM_01	5.61E-08	-18.6734	9.16E-06
17	NM_004390 /// NM_14897	5.15E-08	-18.9137	0.0025766
18	NM_001372 /// NM_00466	1.98E-05	-19.0207	7.30E-08
19	NM_001127381 /// NM_00	0.000111362	-19.0272	0.000508613
20	NM_015675	3.94E-05	-19.0888	0.00643934
21	NM_052972	1.20E-06	-19.1217	6.96E-07
22	NM_001204477 /// NM_00	2.82E-05	-19.1404	0.0370612
23	NM_003246	4.50E-05	-19.1653	5.03E-06
24	NM_004787	9.76E-06	-19.3496	0.00292932
25	NM_000492	0.000204292	-19.3924	0.00459581
26	NM_001145077	1.93E-05	-19.3925	6.46E-07
27	NM_006186 /// NM_17317	5.59E-06	-19.5129	2.02E-05
28	NR_040091 /// NR_040092	3.02E-07	-19.6516	0.00016302
29	NM_001082972 /// NM_00	3.30E-05	-19.8039	0.00778541
30	NM_002487	3.01E-05	-19.8714	0.00866296
31	NM_001128850 /// NM_00	5.71E-05	-19.9522	3.55E-06
32	NM_002943 /// NM_13426	6.29E-06	-20.03	0.00867568
33	NM_020877	9.11E-06	-20.0778	4.82E-05
34	NM_178452	1.12E-07	-20.1865	7.69E-09
35	NM_001128933 /// NM_00	3.47E-07	-20.4688	1.91E-05
36	NM_001080378 /// NM_00	1.85E-06	-20.5181	4.96E-06
37	NM_012307	1.72E-05	-20.7012	2.53E-06
38	NM_001014440	7.96E-05	-20.7364	4.14E-05
39	NM_024763 /// NM_20701	3.06E-05	-20.7507	0.000167718
40	NM_001270041 /// NM_00	7.06E-05	-20.8905	1.15E-05
41	NM_000239	1.12E-05	-21.0375	0.00380823
42	NM_006988	1.42E-06	-21.4052	0.000328286
43	NM_001003809 /// NM_00	0.00026999	-21.6701	0.00126275
44	NM_198469	5.37E-06	-21.6727	8.95E-07
45	NM_001190462	3.05E-05	-21.6779	3.00E-07
46	NM_007335 /// NM_00733	6.15E-06	-21.6806	6.65E-07
47	NM_001270422 /// NM_01	5.85E-05	-21.7474	0.000139775
48	NM_001006655 /// NM_01	8.73E-06	-21.8827	2.75E-05
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1	NM_023037	2.33E-05	-21.8939	0.00275597
2	XR_109470 /// XR_111780	4.65E-08	-21.904	0.00464667
3	NM_000044 /// NM_00101	3.34E-06	-22.012	0.000468651
4	NM_025184	1.03E-06	-22.1724	2.12E-06
5	NM_001204869 /// NM_00	0.000224849	-22.2144	0.0347258
6	NM_001541 /// NM_08065	2.69E-05	-22.4809	0.00683685
7	NM_031476	6.10E-06	-22.603	0.00378904
8	NM_001039766 /// NR_02	2.71E-05	-22.6252	0.00643184
9	NM_001012502	6.47E-06	-22.7319	2.60E-06
10	NM_006290	4.12E-08	-22.7608	3.92E-05
11	NM_153376	3.11E-05	-22.7798	1.44E-05
12	NM_000633 /// NM_00065	1.44E-05	-22.8051	0.0131311
13	NM_001128595 /// NM_00	1.18E-05	-22.8312	0.0278602
14	NM_001039183 /// NM_00	1.99E-06	-22.8807	0.0233671
15	NM_000770 /// NM_00119	0.00015386	-22.9275	0.000886915
16	NM_145235	6.55E-07	-22.9348	9.61E-05
17	NM_001195303 /// NM_00	1.35E-05	-23.0136	0.000305767
18	NM_002122 /// XM_00311	0.00426421	-23.0892	0.000729735
19	NM_024614 /// NR_02680	2.44E-06	-23.4758	0.00344101
20	NM_172365	2.20E-06	-23.4763	1.85E-06
21	NM_001164730 /// NM_00	4.14E-06	-23.4908	1.38E-07
22	NM_207437	2.47E-06	-23.7311	5.25E-07
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26	NM_001204051 /// NM_00	5.69E-06	-24.6319	0.0419278
27	NM_001130090 /// NM_00	1.36E-07	-24.634	9.11E-08
28	NM_000777 /// NM_00119	0.0010862	-24.8372	0.000319805
29	NR_015424	0.00030897	-24.8511	0.0024341
30	NM_030666	4.40E-10	-25.1235	1.03E-07
31	NR_003063	4.12E-06	-25.429	2.59E-07
32	NM_015225 /// NM_13881	3.79E-06	-25.7145	0.0156305
33	NM_003407	6.53E-09	-25.7647	5.09E-06
34	NM_004058 /// NM_08059	0.000412889	-25.9072	0.00291405
35	NM_138788	4.30E-06	-25.9593	3.93E-06
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37	NM_020879	2.16E-05	-26.1866	0.0100483
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47	NM_015964 /// NM_01614	1.59E-06	-27.6943	1.40E-06

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2	NM_001012642	5.95E-07	-27.7714	0.00733639
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4	NM_001243965 /// NM_00	3.56E-08	-28.0359	2.22E-05
5	NM_001199573 /// NM_00	3.62E-08	-28.2653	3.90E-05
6	NM_001170806 /// NM_17	6.41E-05	-28.6611	0.00129192
7	NM_001198542 /// NM_00	6.10E-07	-28.7687	3.42E-07
8	NM_000777 /// NM_00119	1.76E-05	-28.809	0.00068468
9	NM_001100159 /// NM_00	0.00043475	-28.9804	0.000125715
10	NM_000044 /// NM_00101	9.88E-06	-29.1522	0.000918005
11	NM_001831 /// NM_20333	3.62E-07	-29.1919	0.0183023
12	NM_001099677 /// NM_02	4.29E-05	-29.2517	3.17E-05
13	NM_178824	4.12E-05	-29.479	1.27E-06
14	NM_016234 /// NM_20337	1.28E-09	-29.8759	4.34E-08
15	NM_001372 /// NM_00466	2.16E-05	-30.0155	5.00E-07
16	NM_005797 /// NM_14476	9.78E-06	-30.5129	0.0422581
17	NM_031956	1.35E-05	-30.5956	2.60E-07
18	NM_004925	1.13E-05	-30.6119	0.016608
19	NM_024786	1.70E-06	-31.0398	0.00246285
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21	NM_001128850 /// NM_00	4.47E-06	-31.0966	1.22E-07
22	NM_012309 /// NM_13326	2.87E-06	-31.4964	0.0207975
23	NM_001085447	1.22E-05	-32.1166	1.62E-06
24	NM_152750 /// XR_132543	1.35E-06	-32.1978	4.47E-08
25	NM_014466	4.39E-06	-32.3346	0.000140173
26	NM_001008534 /// NM_00	3.94E-05	-32.5418	4.75E-07
27	NM_001039592 /// NM_01	4.77E-06	-32.8687	3.66E-06
28	NM_001114938 /// NM_00	1.66E-06	-32.9932	4.25E-08
29	NM_001172810 /// NM_02	9.01E-07	-33.0847	3.60E-09
30	NM_000062 /// NM_00103	1.14E-07	-33.2161	0.0161282
31	NM_005252	8.72E-06	-33.2807	4.99E-05
32	NM_033413	2.41E-06	-33.4309	3.75E-08
33	NM_130446	6.23E-06	-33.4314	1.62E-06
34	NM_001135091 /// NM_00	0.000217009	-33.4666	0.00264031
35	NM_144715	1.23E-05	-33.8252	6.20E-07
36	NM_001243965 /// NM_00	4.92E-07	-34.0139	0.000441615
37	NM_030820	1.35E-05	-34.0542	4.09E-08
38	NM_001920 /// NM_13350	1.08E-05	-34.242	0.00166842
39	NM_033413	3.38E-07	-34.465	5.33E-09
40	NM_012309 /// NM_13326	1.32E-06	-34.4686	0.00873723
41	NM_002089	9.70E-05	-35.1846	5.03E-08
42	NM_152750 /// XR_132543	5.10E-07	-35.7083	1.19E-08
43	NM_031457	1.81E-05	-35.8343	5.40E-07
44	NM_001206897 /// NM_00	3.92E-08	-35.8876	1.12E-07
45	NM_001243965 /// NM_00	2.22E-07	-35.8911	7.22E-05
46	NM_001831 /// NM_20333	1.10E-07	-36.0344	0.0210951
47	NM_001199633 /// NM_02	1.53E-06	-36.1055	5.00E-05
48	NM_001040092 /// NM_00	1.27E-06	-36.4716	3.39E-06

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2	NM_014265 /// NM_02177	4.86E-06	-36.5621	0.000737601
3	NM_020225	2.21E-08	-36.7186	0.00813845
4	NM_199280	5.33E-07	-37.0838	1.66E-07
5	NM_001263	2.27E-06	-37.7801	0.00143123
6	NM_181643	1.52E-07	-38.1709	1.99E-07
7	NM_001105248 /// NM_00	5.22E-06	-38.7019	1.16E-05
8	NM_004058 /// NM_08059	5.10E-06	-39.272	0.00103517
9	NM_001243115 /// NM_02	4.09E-05	-39.5179	7.72E-05
10	NM_152665	4.52E-05	-39.7574	8.98E-07
11	NM_001263	6.29E-06	-39.8588	0.00232381
12	NM_012309 /// NM_13326	0.000100395	-39.9057	0.0346321
13	NM_001143941 /// NM_00	6.65E-05	-40.2316	0.000299831
14	NM_001002029 /// NM_00	2.24E-06	-40.8773	0.000595415
15	NM_001112717 /// NM_00	1.11E-08	-41.7871	0.000474851
16	NM_001142958 /// NM_15	2.18E-06	-41.9092	4.97E-06
17	NM_024677	4.88E-06	-42.199	0.0427014
18	NM_173081	2.83E-05	-42.512	9.37E-06
19	NM_032445	3.85E-06	-43.5731	6.68E-08
20	NM_001243965 /// NM_00	2.00E-06	-44.0241	0.000469459
21	NM_025244 /// NM_18291	4.28E-06	-44.1898	1.90E-06
22	NM_001013625	3.54E-06	-44.643	3.04E-06
23	NM_001831 /// NM_20333	5.03E-08	-44.8306	0.013923
24	NM_003014	4.19E-05	-45.3445	8.18E-05
25	NM_007168	1.60E-05	-45.4576	2.43E-06
26	NM_001267798 /// NM_00	2.61E-06	-45.6727	0.000156118
27	NM_004482	3.82E-09	-45.9695	0.00568869
28	NM_001205288 /// NM_03	9.45E-06	-46.4919	0.0115039
29	NM_001242524 /// NM_00	6.61E-06	-46.963	0.000306226
30	NM_206996	1.21E-06	-47.0058	7.39E-06
31	NM_058187	9.06E-09	-47.0844	0.000165226
32	NM_000926 /// NM_00120	0.000292803	-47.2619	0.00060646
33	NM_001079855 /// NM_00	5.71E-06	-52.314	0.0432543
34	NM_005160	4.96E-08	-52.3613	0.0068473
35	NM_144992	1.51E-05	-54.099	3.79E-07
36	NM_001142302 /// NM_01	0.000241993	-54.4723	0.0030382
37	NM_001244134 /// NM_00	8.86E-09	-54.751	0.000142616
38	NM_000104	1.76E-08	-56.7041	0.000120721
39	NM_001128933 /// NM_00	1.78E-06	-56.9467	5.37E-05
40	NM_145263	6.01E-05	-57.717	1.49E-06
41	NM_001252195 /// NM_03	3.07E-08	-58.5808	9.98E-10
42	NM_024763 /// NM_20701	4.44E-05	-58.9127	0.000443031
43	NM_000204	4.34E-09	-59.0591	5.13E-06
44	NM_001172105 /// NM_01	7.56E-07	-59.5388	0.0197709
45	NM_000065 /// NM_00111	4.16E-09	-61.4678	1.34E-11
46	NM_145170	1.92E-05	-61.7455	0.000132385
47	NM_001145399 /// NM_00	4.39E-05	-62.6275	0.013254

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2	NM_001105248 /// NM_00	1.02E-06	-63.1097	3.08E-05
3	NM_031421	1.78E-08	-64.6176	1.50E-08
4	NM_014722 /// NM_01586	8.91E-08	-67.0458	7.24E-09
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6	NM_024694	7.31E-07	-68.4132	5.15E-09
7	NM_001114171 /// NM_00	4.51E-05	-69.1993	6.43E-05
8	NM_001030287 /// NM_00	3.83E-05	-69.4149	0.000256797
9	NM_001145033	6.89E-06	-70.8927	0.000539685
10	NM_001002029 /// NM_00	2.50E-07	-71.1309	0.000477062
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13	NM_033364 /// XR_132494	6.16E-11	-73.0893	8.35E-06
14	NM_001199201 /// NM_00	7.94E-08	-73.1336	3.72E-09
15	NM_001077710	5.80E-11	-73.8673	2.78E-05
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17	NM_001128304 /// NM_00	3.90E-07	-76.474	0.0283374
18	NM_000208 /// NM_00107	5.73E-12	-77.5206	0.00176242
19	NM_001010940	7.75E-05	-78.8243	2.95E-05
20	NM_001008226	3.10E-06	-82.7256	8.82E-08
21	NM_021229	1.08E-07	-84.3761	0.0396582
22	NM_024870 /// NM_02517	2.77E-06	-87.5465	0.00194562
23	NM_176813	2.85E-06	-87.8292	2.00E-07
24	NM_001253835 /// NM_00	1.84E-07	-90.9671	0.00610231
25	NM_024783	4.59E-07	-92.5521	2.49E-07
26	NM_178456	2.25E-07	-94.1098	6.78E-09
27	NM_130897	1.43E-06	-96.9537	2.21E-07
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29	NM_024867 /// NM_14472	3.58E-07	-106.666	1.10E-06
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33	NM_001165963 /// NM_00	1.20E-08	-117.312	2.39E-11
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35	NM_152321	9.88E-07	-121.764	0.000221113
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37	NM_178504 /// NM_19856	1.23E-06	-132.326	1.06E-07
38	NM_000877	8.91E-09	-136.757	0.0123422
39	NM_001004303	3.19E-06	-143.205	6.02E-07
40	NM_152548	1.78E-06	-151.774	1.86E-06
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42	NM_001142407 /// NM_00	2.92E-10	-161.399	8.24E-13
43	NM_145170	2.01E-08	-176.685	0.000107506
44	NM_000699 /// NM_00100	2.94E-08	-222.123	0.00185847
45	NM_080860	3.27E-09	-232.023	3.07E-06
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38	2.90322
39	3.16162
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2 Supplementary Table 4 aberrantly upregulated in common between STIC and invasive cancer (2 fold and
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Gene Symbol	RefSeq	Invasive SC vs. Normal oviduct		STIC vs. Normal oviduct
		p-value	Fold-Change	
ASPM	NM_018136	2.60E-06	2.94409	1.33E-05
CCDC144A	ENST00000443444	0.00213885	5.32473	0.0243328
CCNE1	ENST00000262643	0.00572145	2.23008	0.0115957
CDH6	NM_004932	0.00283368	2.1433	0.000295215
CENPF	NM_016343	5.58E-07	3.37557	2.40E-06
CKS2	NM_001827	0.0022546	2.89973	0.001283
CLDN6	ENST00000396925	0.0104175	5.93699	0.00243631
CLIC5	NM_001114086	0.009439	2.46718	0.00139079
CRABP2	NM_001878	0.00755329	2.78862	0.0212031
DBN1	NM_004395	2.24E-05	2.05241	2.64E-05
DEK	ENST00000397239	0.000384725	2.32674	0.000217432
DNAJB6	ENST00000262177	0.000272738	2.54209	0.00312649
ECT2	NM_001258316	0.000212608	2.53965	0.00013513
FIGN	ENST00000333129	0.0097029	2.50304	0.00128213
FN1	ENST00000354785	0.00215023	4.76499	0.0446495
GINS1	NM_021067	0.00684686	2.17969	0.0074439
HIST1H2AE	NM_021052	3.44E-05	3.19263	0.000221535
HIST1H2BC	NM_003526	0.0198544	2.24863	0.0371524
HIST1H2BK	NM_080593	0.000451902	2.85981	0.00053831
HIST1H2BO	NM_003527	0.00192634	2.62733	0.00989244
HIST1H3F	NM_021018	0.00448196	3.10484	0.00305663
HIST1H4C	NM_003542	0.00833898	2.18377	0.00595323
HIST1H4L	NM_003546	0.000243457	3.58937	0.000175076
HIST2H2AB	NM_175065	0.000637198	4.20247	0.000722952
KPNA2	NM_002266	0.00344636	2.34762	0.0129578
LOC441268	AK125166	0.000374969	4.11755	0.000820112
MACC1	NM_182762	0.0304047	2.35567	0.0382608
MKI67	ENST00000368654	0.00039812	2.5419	0.000512702
MMP23B	NM_006983	0.0129185	2.51867	0.00175544
MT1G	ENST00000444837	0.0428614	2.35685	0.00461934
NREP	NM_001142481	0.000485486	3.15952	0.00240787
PHOSPHO2-KLHL23	NM_001199290	0.000554576	2.64251	0.00116485
PRAME	NM_206953	0.0297283	2.12296	0.00542624
PRC1	ENST00000361188	0.000336928	2.21306	0.000736568
PTH2R	NM_005048	0.00495188	2.23137	0.00544872
PTTG1	ENST00000352433	0.00451955	2.80642	0.0390721
PVRL3	NM_015480	0.00765987	2.68279	0.0137273
RPL39L	ENST00000296277	0.0055029	2.62684	0.00333233
RRM2	ENST00000360566	0.00383353	2.68346	0.0128528
SKIL	NM_005414	0.0130943	2.03889	0.00849818
SLC16A1	NM_001166496	0.00557925	2.30772	0.0072816
SLC38A1	NM_030674	0.0010424	2.31448	0.0024103
SMC4	NM_005496	4.93E-05	2.57383	0.000371199

1	SPINT2	NM_021102	0.000296385	2.21178	0.000238397
2	STMN1	NM_203401	4.99E-06	3.48098	8.76E-07
3	TBL1XR1	ENST00000430069	0.0174733	2.05526	0.0189784
4	TIA1	NM_022037	0.00310822	2.37	0.00490998
5	TMSB10	NM_021103	3.32E-05	2.60096	2.32E-05
6	TOP2A	NM_001067	0.0001045	3.28641	0.000712484
7	TPMT	NM_000367	0.0107081	2.62068	0.0237245
8	TPX2	NM_012112	4.09E-05	3.27148	0.000258971
9	TXND9	NM_005783	0.00363903	2.0506	0.00286028
10	UBE2T	ENST00000367274	0.0043026	2.33065	0.00586935
11	URI1	ENST00000542441	0.0130175	2.43578	0.00507933
12	WRAP53	ENST00000316024	0.00287094	2.78275	0.00691762
13	ZC3HAV1L	BC020784	0.00870664	2.10747	0.0106318
14	ZIC1	ENST00000282928	0.0108722	2.60269	0.00477505
15	ZNF146	NM_007145	0.00509871	2.49424	0.00149398
16	ZNF345	NR_038362	0.00010634	2.33358	0.000569311
17	ZNF566	NM_001145345	0.000363159	2.17544	0.000559765
18	ZNF850	NM_001193552	0.000890238	2.03178	7.58E-05
19	ZNF93	NM_031218	0.00124937	3.25181	0.000421892
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4 Fold-Change
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7 3.10055
8 2.04568
9 2.72304
10 2.94353
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2 Supplementary Table 5 overlapped genes between immortalized and STIC (123 genes)-upregulated
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5	Gene Symbol	Gene Title
6	STMN1	stathmin 1
7	ZNF93	zinc finger protein 93
8	DCDC2	doublecortin domain containing 2
9	CENPF	centromere protein F, 350/400kDa (mitosin)
10	RPL39L	ribosomal protein L39-like
11	CDH6	cadherin 6, type 2, K-cadherin (fetal kidney)
12	RBBP4	Retinoblastoma binding protein 4
13	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)
14	ECT2	epithelial cell transforming sequence 2 oncogene
15	TOP2A	topoisomerase (DNA) II alpha 170kDa
16	NREP	neuronal regeneration related protein homolog (rat)
17	ASPM	asp (abnormal spindle) homolog, microcephaly associated
18	FN1	(Drosophila) fibronectin 1
19	CDH2	cadherin 2, type 1, N-cadherin (neuronal)
20	MKI67	antigen identified by monoclonal antibody Ki-67
21	ZC3H11A	zinc finger CCCH-type containing 11A
22	UBE2T	ubiquitin-conjugating enzyme E2T (putative)
23	SMC4	structural maintenance of chromosomes 4
24	SKIL	SKI-like oncogene
25	ARHGAP29	Rho GTPase activating protein 29
26	CXCR4	chemokine (C-X-C motif) receptor 4
27	ZNF644	zinc finger protein 644
28	PRC1	protein regulator of cytokinesis 1
29	EPB41L5	erythrocyte membrane protein band 4.1 like 5
30	MSH2	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
31	UBE2C	ubiquitin-conjugating enzyme E2C
32	MASTL	microtubule associated serine/threonine kinase-like
33	KIF23	kinesin family member 23
34	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)
35	STAT1	signal transducer and activator of transcription 1, 91kDa
36	NUSAP1	nucleolar and spindle associated protein 1
37	PARP14	poly (ADP-ribose) polymerase family, member 14
38	TTK	TTK protein kinase
39	KPNA4	karyopherin alpha 4 (importin alpha 3)
40	ANP32E	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E
41	CEP55	centrosomal protein 55kDa
42	CCDC88A	coiled-coil domain containing 88A
43	KIF20B	kinesin family member 20B
44	CREB1	cAMP responsive element binding protein 1
45	SYT11	synaptotagmin XI
46	IFIT2	interferon-induced protein with tetratricopeptide repeats 2
47	CDKN3	cyclin-dependent kinase inhibitor 3
48	PLEKHO1	pleckstrin homology domain containing, family O member 1

1	NDC80	NDC80 kinetochore complex component homolog (S. cerevisiae)
2	CHEK1	checkpoint kinase 1
3	PEA15	phosphoprotein enriched in astrocytes 15
4	FOXM1	forkhead box M1
5	KLHL24	kelch-like 24 (Drosophila)
6	KALRN	kalirin, RhoGEF kinase
7	SKA3	spindle and kinetochore associated complex subunit 3
8	CARD16	caspase recruitment domain family, member 16
9	CKAP2	cytoskeleton associated protein 2
10	CGGBP1	CGG triplet repeat binding protein 1
11	IFI44	interferon-induced protein 44
12	ANLN	anillin, actin binding protein
13	STAT2	signal transducer and activator of transcription 2, 113kDa
14	RAI14	retinoic acid induced 14
15	EMP1	epithelial membrane protein 1
16	KIF11	kinesin family member 11
17	CDK1	Cyclin-dependent kinase 1
18	NUF2	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)
19	NABP1	nucleic acid binding protein 1
20	KIF18A	kinesin family member 18A
21	PRKD3	protein kinase D3
22	MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2
23	PTMS	parathymosin
24	SPECC1	sperm antigen with calponin homology and coiled-coil domains 1
25	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2
26	PRTFDC1	phosphoribosyl transferase domain containing 1
27	KIAA1524	KIAA1524
28	PTBP2	polypyrimidine tract binding protein 2
29	KIAA0101	KIAA0101
30	PTPN14	protein tyrosine phosphatase, non-receptor type 14
31	FBXO28	F-box protein 28
32	MX2	myxovirus (influenza virus) resistance 2 (mouse)
33	NCAPG	non-SMC condensin I complex, subunit G
34	CEP89	centrosomal protein 89kDa
35	CNPY3	canopy 3 homolog (zebrafish)
36	RIF1	RAP1 interacting factor homolog (yeast)
37	ATAD2	ATPase family, AAA domain containing 2
38	CALU	calumenin
39	FADS2	fatty acid desaturase 2
40	SLC16A4	solute carrier family 16, member 4 (monocarboxylic acid transporter 5)
41	ENPP5	ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative)
42	BMPR2	bone morphogenetic protein receptor, type II (serine/threonine kinase)
43	SLC30A6	solute carrier family 30 (zinc transporter), member 6
44	ARHGAP11A	Rho GTPase activating protein 11A
45	LMO4	LIM domain only 4
46	RAB23	RAB23, member RAS oncogene family
47	BCAP29	B-cell receptor-associated protein 29

1	DTL	denticleless E3 ubiquitin protein ligase homolog (Drosophila)
2	CLIC4	chloride intracellular channel 4
3	TLK2	tousled-like kinase 2
4	CDC5L	CDC5 cell division cycle 5-like (S. pombe)
5	CDK2	cyclin-dependent kinase 2
6	KLHL14	kelch-like 14 (Drosophila)
7	C12orf4	chromosome 12 open reading frame 4
8	CCDC77	coiled-coil domain containing 77
9	DPYSL3	dihydropyrimidinase-like 3
10	CTHRC1	collagen triple helix repeat containing 1
11	MLF1IP	MLF1 interacting protein
12	TRMT6	tRNA methyltransferase 6 homolog (S. cerevisiae)
13	NCAPH	non-SMC condensin I complex, subunit H
14	ZNF302	zinc finger protein 302
15	ZBTB2	zinc finger and BTB domain containing 2
16	PLEKHG4B	pleckstrin homology domain containing, family G member 4B
17	SGOL2	shugoshin-like 2 (S. pombe)
18	FGF12	fibroblast growth factor 12
19	HERC5	HECT and RLD domain containing E3 ubiquitin protein ligase 5
20	RFC3	replication factor C (activator 1) 3, 38kDa
21	FBXO5	F-box protein 5
22	PARPBP	PARP1 binding protein
23	DKK3	dickkopf 3 homolog (Xenopus laevis)
24	STAU2	staufen, RNA binding protein, homolog 2 (Drosophila)
25	SEC22B	SEC22 vesicle trafficking protein homolog B (S. cerevisiae) (gene/pseudogene)
26	RAD1	RAD1 homolog (S. pombe)
27	KIAA0355	KIAA0355
28	CCNA2	cyclin A2
29	RNF144A	ring finger protein 144A
30	STIL	SCL/TAL1 interrupting locus
31	MSH6	mutS homolog 6 (E. coli)
32	MCM4	minichromosome maintenance complex component 4
33	TMPO	thymopoietin
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Immnortalized vs. normal SC		STIC vs. normal oviduct	
p-value	Fold-Change	p-value	Fold-Change
0.000283907	3.80725	8.76E-07	4.23057
0.0144245	2.87429	0.000421892	3.8168
0.00716298	13.1974	4.28E-06	2.99104
0.00282425	4.4932	2.40E-06	2.94353
0.0472861	2.37036	0.00333233	2.82552
0.000144791	16.6572	0.000295215	2.72304
0.0360557	2.07024	0.00182861	2.69556
0.0155442	3.41929	0.000258971	2.67713
0.000987003	2.69336	0.00013513	2.65618
0.0384599	3.66365	0.000712484	2.63066
0.049286	3.34473	0.00240787	2.57426
0.00995083	4.19182	1.33E-05	2.55218
0.000815221	7.51886	0.0446495	2.52238
0.00103662	26.8722	0.0442521	2.48339
0.00406514	2.92177	0.000512702	2.47644
0.0440437	2.07644	0.0102092	2.2883
0.0146618	2.60053	0.00586935	2.2434
0.021717	2.65716	0.000371199	2.15717
8.38E-06	6.69368	0.00849818	2.15188
0.000667348	6.11737	0.0160522	2.12452
0.000441767	12.0686	0.0203638	2.07604
0.00479026	2.08711	0.000646319	2.06913
0.0472451	3.40855	0.000736568	2.06902
0.0184493	3.71605	0.00312586	2.05776
0.0384693	3.04204	0.0062282	2.03844
0.00446833	3.63974	0.000282922	2.01489
0.0176956	3.4969	0.000964698	2.00404
0.0424054	3.89455	0.000618361	1.99464
0.00893113	4.51362	0.000357272	1.98425
0.0104007	12.2952	0.00151445	1.9638
0.00123492	4.91539	0.000469143	1.96106
0.000783412	7.93847	0.0084577	1.95012
0.0196974	2.55622	0.000316293	1.94746
0.00158105	3.71015	8.16E-05	1.94129
0.0462063	2.82448	0.00638506	1.91164
0.0390095	4.1117	0.00165101	1.90968
0.000140019	2.80443	2.09E-05	1.88932
0.000216432	2.09166	9.57E-05	1.88057
0.0314904	2.44408	0.00629166	1.87344
0.00807315	12.0806	0.000205062	1.8629
0.00426074	14.3947	0.0229778	1.84615
0.0101394	3.42749	0.0075941	1.84499
0.0253665	2.86124	0.00881319	1.84464

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2	0.0126441	5.27019	7.79E-05	1.83858
3	0.0191874	2.34074	0.00149298	1.83041
4	0.000268136	3.21355	0.00114403	1.82733
5	0.00369879	4.15964	0.00984894	1.8245
6	0.00407175	9.06502	0.00275194	1.82414
7	0.00083655	2.66607	0.000161309	1.80456
8	0.00520891	2.8186	1.07E-05	1.80031
9	0.0423289	3.741	0.0312376	1.79989
10	0.00469199	2.15955	0.00958603	1.79114
11	0.00550966	3.07566	0.0131361	1.78867
12	0.00161764	29.8796	0.0440225	1.77371
13	0.0130951	3.04741	0.00422736	1.76301
14	0.00875975	3.33513	0.00664215	1.75298
15	0.030317	3.5904	0.0100821	1.75181
16	0.039396	2.08173	0.0327551	1.74284
17	0.0428742	3.36452	0.000875107	1.73854
18	0.000234549	2.73747	0.0112627	1.73794
19	0.00183276	3.97249	0.00489193	1.737
20	0.00405556	3.08255	0.00350044	1.72237
21	0.00648228	2.47888	0.000740851	1.72116
22	0.00201868	3.3178	0.00488377	1.71706
23	0.00170041	2.14286	0.0218899	1.71534
24	0.0420002	2.24513	0.000834693	1.69995
25	0.0222086	2.49395	0.00973343	1.69965
26	5.14E-07	4.83426	0.00898711	1.6906
27	0.0209858	6.32114	5.02E-05	1.69015
28	0.000189528	6.15731	0.000338866	1.6883
29	0.00106914	2.11285	0.0205669	1.6871
30	0.0248471	3.29181	0.0408938	1.68567
31	0.000925396	2.37864	0.0244379	1.6841
32	0.0332968	2.00636	0.00621127	1.68318
33	4.11E-05	36.5634	0.0399436	1.68097
34	0.00692782	4.49406	0.000777004	1.67433
35	0.00588523	2.36836	0.00711967	1.67311
36	0.0111908	2.40382	0.00215059	1.67212
37	0.0335808	2.02439	0.00316773	1.67174
38	0.0230576	3.44623	0.00395446	1.66638
39	0.00520529	4.23804	0.0027015	1.64975
40	3.08E-06	3.2561	0.00322815	1.64855
41	1.07E-05	6.74615	0.00813651	1.64756
42	0.0200538	8.15037	0.0468952	1.64689
43	0.000752569	2.35956	0.0274736	1.6438
44	0.0188408	2.02722	0.0017683	1.64325
45	0.00178417	2.5401	0.00899648	1.63703
46	0.0476972	2.86426	0.000987487	1.6358
47	2.44E-06	3.29664	0.00897206	1.63094
48	0.0410158	2.72067	0.00775898	1.62293
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1	0.000617135	3.98727	0.00333312	1.62264
2	0.000602153	2.56418	0.0415462	1.6206
3	0.0436593	2.17529	0.0317785	1.6142
4	0.00100088	2.80715	0.0137566	1.61287
5	0.00630406	3.30955	0.0152348	1.61234
6	0.00367269	7.16821	0.0129579	1.61218
7	0.00724886	2.49163	0.0120534	1.61084
8	0.0465192	3.49878	0.000262927	1.60787
9	0.000118014	6.52417	0.0144391	1.59572
10	0.00549029	23.5167	0.0435348	1.58698
11	0.00074259	5.44894	0.00331259	1.57913
12	0.0147488	2.36385	0.0119903	1.57533
13	0.0109051	3.06047	0.00160924	1.57371
14	0.00872522	3.98681	0.00845558	1.57159
15	0.0254929	2.60135	0.0224159	1.56814
16	0.0150965	5.70056	0.00541019	1.55604
17	0.00666477	3.6087	1.00E-05	1.55527
18	0.0102868	2.52622	0.000725724	1.55182
19	1.57E-05	36.887	0.000644676	1.55154
20	0.0149205	2.13383	0.00265562	1.55106
21	0.046043	3.54316	0.00136405	1.54256
22	0.00316853	3.11433	0.000703062	1.53346
23	0.0339119	6.37923	0.0115379	1.52728
24	0.0387225	3.03602	0.00145672	1.52095
25	0.00153509	3.00068	0.0302589	1.51537
26	0.0113217	3.63938	0.00658345	1.51434
27	0.0117881	2.80383	0.00519076	1.51323
28	0.00595046	2.98481	0.0429142	1.51204
29	0.00866395	4.28053	0.00252979	1.51191
30	0.00235006	4.79982	0.00112532	1.51049
31	0.00172162	2.58461	0.0267306	1.50822
32	0.000521248	2.55083	0.0327635	1.50167
33	0.00251306	2.71931	0.00420601	1.50058

The PAX2-null immunophenotype defines multiple lineages with common expression signatures in benign and neoplastic oviductal epithelium

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Abstract

The oviducts contain high-grade serous cancer (HGSC) precursors (serous tubal intraepithelial neoplasia or STINs), which are γ -H2AX^p- and TP53 mutation-positive. Although they express wild-type p53, secretory cell outgrowths (SCOUTs) are associated with older age and serous cancer; moreover, both STINs and SCOUTs share a loss of PAX2 expression (PAX2ⁿ). We evaluated PAX2 expression in proliferating adult and embryonic oviductal cells, normal mucosa, SCOUTs, Walthard cell nests (WCNs), STINs, and HGSCs, and the expression of genes chosen empirically or from SCOUT expression arrays. Clones generated *in vitro* from embryonic gynaecological tract and adult Fallopian tube were Krt7^p/PAX2ⁿ/EZH2^p and underwent ciliated (PAX2ⁿ/EZH2ⁿ/FOXJ1^p) and basal (Krt7ⁿ/EZH2ⁿ/Krt5^p) differentiation. Similarly, non-ciliated cells in normal mucosa were PAX2^p but became PAX2ⁿ in multi-layered epithelium undergoing ciliated or basal (WCN) cell differentiation. PAX2ⁿ SCOUTs fell into two groups: type 1 were secretory or secretory/ciliated with a 'tubal' phenotype and were ALDH1ⁿ and β -catenin^{memb} (membranous only). Type 2 displayed a columnar to pseudostratified (endometrioid) phenotype, with an EZH2^p, ALDH1^p, β -catenin^{nc} (nuclear and cytoplasmic), stathmin^p, LEF1^p, RCN1^p, and RUNX2^p expression signature. STINs and HGSCs shared the type 1 immunophenotype of PAX2ⁿ, ALDH1ⁿ, β -catenin^{memb}, but highly expressed EZH2^p, LEF1^p, RCN1^p, and stathmin^p. This study, for the first time, links PAX2ⁿ with proliferating fetal and adult oviductal cells undergoing basal and ciliated differentiation and shows that this expression state is maintained in SCOUTs, STINs, and HGSCs. All three entities can demonstrate a consistent perturbation of genes involved in potential tumour suppressor gene silencing (EZH2), transcriptional regulation (LEF1), regulation of differentiation (RUNX2), calcium binding (RCN1), and oncogenesis (stathmin). This shared expression signature between benign and neoplastic entities links normal progenitor cell expansion to abnormal and neoplastic outgrowth in the oviduct and exposes a common pathway that could be a target for early prevention.

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Introduction

Recent discoveries have strengthened the relationship between the distal Fallopian tube and epithelial malignancies traditionally attributed to the ovary, specifically high-grade serous carcinomas (HGSCs), the most lethal of ovarian cancers [1–3]. With these discoveries has emerged a collective effort to resolve the sequence of histological and molecular events giving rise to these

tumours in the Fallopian tube. The serous carcinogenic sequence involves not only frank malignancies with metastatic spread, but also serous cancer precursors, including latent precursors – the p53 signature – and serous tubal intraepithelial neoplasms (STINs). The latter include intramucosal carcinomas (STICs) and lesser but immunophenotypically similar atypias that are considered premalignant intraepithelial lesions (STILs) [4,5]. Virtually all serous cancer precursors

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contain mutations in *TP53*, evidence of a DNA damage response (γ -H2AX^P), and predominate in the distal Fallopian tube [4]. Contiguous benign (p53 signatures) and malignant (STICs) epithelia have been documented with shared mutations in specific codons of *TP53* [4,6]. In addition, further studies have unearthed other benign epithelial alterations, termed secretory cell outgrowths (SCOUTs), that do not contain *TP53* mutations or evidence of a DNA damage response, yet share with precursors and carcinomas loss of PAX2 expression [7–9]. SCOUTs do not appear directly linked to HGSC, but have been documented at higher frequency in the normal tubes of postmenopausal women and those with HGSC [8,9]. Based on these properties, we have designated SCOUTs as 'surrogate precursors' and hypothesize that both SCOUTs and serous cancer precursors share properties or similar mechanisms in their pathogenesis, albeit with different potential outcomes.

The shared loss of PAX2 expression in both SCOUTs and many 'true' serous cancer precursors suggests that inactivation of this gene, while integral to neoplasia, has a wider range of associations and may signify a generic pathway common to epithelial cell expansion. The goals of this study were, firstly, to determine the breadth of the PAX2ⁿ immunophenotype in the Fallopian tube by examining 'normal' cell growth and differentiation *in vitro* and *in vivo*. Secondly, we wanted to characterize more fully the alterations in expression that typified SCOUTs by array analysis and employ a biomarker

profile to determine whether the SCOUT signature was recapitulated in STINs and HGSCs.

Materials and methods

Case material

This study was approved by the Brigham and Women's Human Investigation Committee and involved the use of discarded fresh and archived tissues. Case material for antibody staining consisted of the following epithelia/lesions: (1) normal salpingeal epithelium ($n = 15$); (2) SCOUTs ($n = 44$) and other outgrowths such as transitional-like metaplasia [Walthard cell nests (WCNs), $n = 5$]; (3) serous tubal intraepithelial neoplasms (STINs) ($n = 18$); and (4) metastatic or invasive serous carcinomas ($n = 39$). In addition, cultured clonal cells from normal Fallopian tubes were examined for selected marker expression. Cases for immunohistochemistry were selected by one of us (CPC) using previously described criteria (Figure 1) [10].

Cell culture

Fimbrial tissue was obtained from discarded surgical specimens of women undergoing benign procedures. Discarded fetal oviductal tissues were obtained by parental consent under an approved IRB protocol. Disaggregated cells were cultivated onto a feeder layer

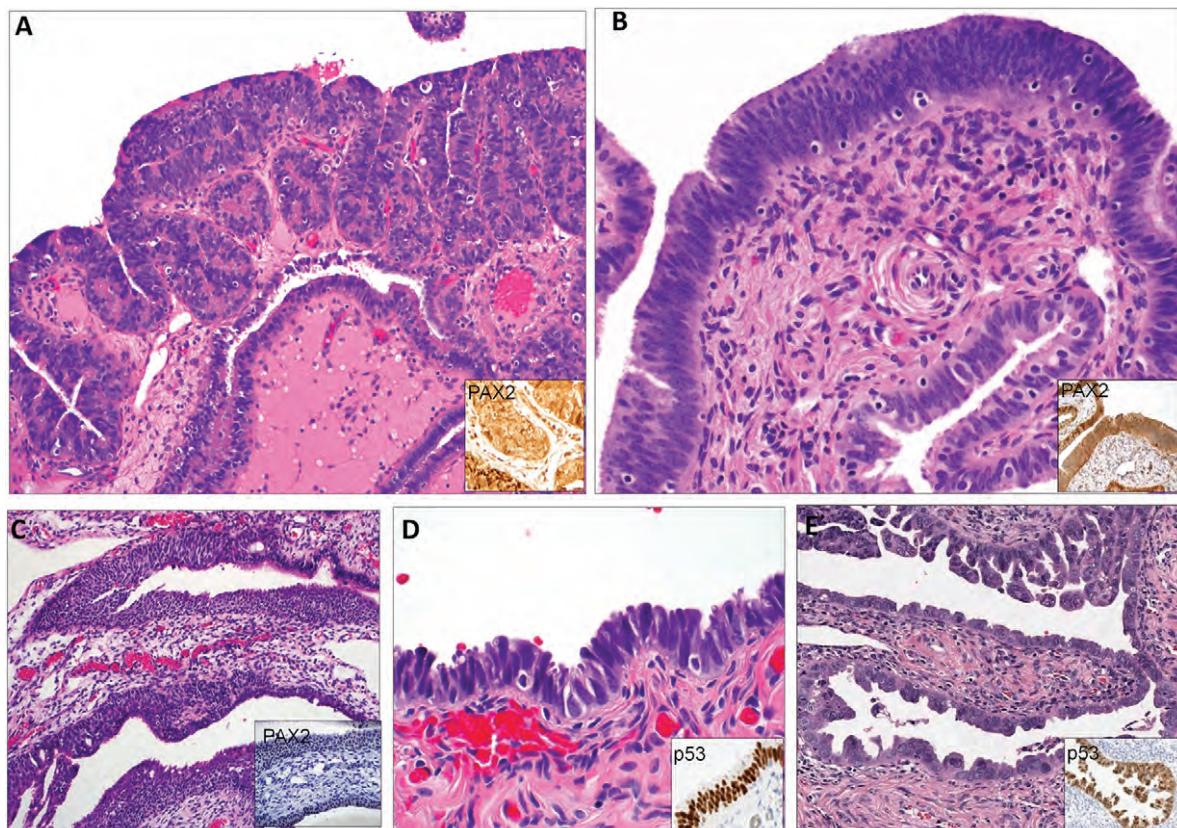


Figure 1. Entities associated with the PAX2ⁿ immunophenotype included (A) type 1 secretory cell outgrowths (SCOUTs), (B) type 2 SCOUTs, (C) Walthard cell nests, and (D) low- and (E) high- (serous tubal intraepithelial carcinoma) grade tubal intraepithelial neoplasia.

of lethally irradiated 3 T3-J2 cells in stem cell culturing media (Jackson Laboratory, scm003). Clonal analysis and *in vitro* 3D differentiation were based on previously described methods for lung epithelial stem cells [11].

Microarray and bioinformatics

In order to identify genes expressed in PAX2ⁿ epithelium, expression arrays were generated from formalin-fixed, laser-capture-micro-dissected (LCM) PAX2ⁿ SCOUTs and benign control oviductal epithelium. RNAs obtained from the LCM procedure were amplified using the Ovation FFPE WTA System, WT-Ovation Exon Module, and Encore Biotin Module (NuGEN Technologies, San Carlos, CA, USA) and hybridized onto GeneChip® Human Exon 1.0 ST Arrays. GeneChip operating software was used to process all the Cel files and calculate probe intensity values. To validate sample quality, hybridization ratios were calculated using Affymetrix Expression Console software. The intensity values were log₂-transformed and imported into the Partek Genomics Suite. Exons were summarized to genes and a one-way ANOVA was performed to identify differentially expressed genes. *p* values and fold change were calculated for each analysis. Heat maps were generated using Pearson's correlation and Ward's method with selected genes based on *p* value. Pathway analyses were performed using Gene Set Enrichment Analysis (GSEA) software. Candidate biomarkers were culled from these arrays and are summarized in Supplementary Table 1.

Immunohistochemistry

Immunostaining was performed with attention to the biomarkers in Supplementary Table 1, in which product information and dilutions are included. When normal-appearing epithelia were scanned for putative PAX2ⁿ secretory cells, sections were immunostained with two antibodies concurrently: PAX2, which stains non-ciliated cells, and FOXJ1, a ciliated cell marker. Antibodies to leukocyte common antigen (LCA) for CD3, as well as FASCIN, were also used to track intraepithelial lymphocytes and dendritic cells, which are normally PAX2ⁿ. Detection was completed with the Vectastain ABC kit (Cat No PK-6102; Vector Laboratories, Inc, Burlingame, CA, USA) with a liquid DAB-plus substrate kit (Cat No 00-2020). Slides were counterstained with Hematoxylin Stain 3 (Cat No CS402-1D). Antibody information is summarized in Supplementary Table 1. Reaction to antibody staining is indicated by superscripted 'p' or 'n' for positive or negative (PAX2, ALDH1, FOXJ1, etc), superscripted 'm' or 'wt' for mutated or wild type (p53), and superscripted 'nc' or 'mem' for nuclear and cytoplasmic versus membrane localization (β -catenin). Immunohistochemistry, immunofluorescence staining, and image acquisition were performed as previously described [9,11]. Proliferating clones were identified and immunostained for PAX2, PAX8, FOXJ1, Krt7, Krt5, p63, EZH2,

and Ki67. Evidence of ciliated cell differentiation was identified by immunostaining for FOXJ1 and acetylated alpha-tubulin. Basal cells were identified by Krt5 or p63 immunostaining.

Results

Histological sub-classification of SCOUTs and STINs

The lesions under study are illustrated in Figure 1. Based on previous studies, SCOUTs were subdivided into two general histological categories [8,12]. The first, designated as type 1 SCOUTs, consisted of a typical mono- or bi-phasic tubal epithelial composition with either single layers of tubal non-ciliated cells or (more commonly) a combination of non-ciliated and ciliated cells. The second, arbitrarily labelled type 2 SCOUTs, consisted of proliferations with mildly pseudostratified and closely arranged elongated fusiform nuclei, similar to endometrial epithelium, and also termed 'endometrioid' SCOUTs. Cells with ciliated differentiation (FOXJ1^p) were present, but were typically less than 30% of the cells and scattered throughout the epithelium. Walthard cell nests (WCNs), consisting of basal cell outgrowth with a squamo-transitional phenotype, were also studied because they signify another form of outgrowth derived from columnar epithelial cells, albeit metaplastic. STINs were sub-classified as previously described and contained strong p53 immunostaining and evidence of DNA damage by H2AX staining [5]. Those with mild or moderate atypia and preserved epithelial polarity were classified as low grade and are identical to lesions classified as 'STILs', 'TILTs', and atypical hyperplasia in other reports [13–15]. Those with conspicuous loss of epithelial polarity were classified as high grade, synonymous with serous tubal intraepithelial carcinoma (STIC). The latter have a 0–11% outcome risk of HGSC, based on recent studies [16–18]. The HGSC outcome risk of lower-grade STINs is unknown but presumed to be less than that of high-grade STINs.

In vitro and *in vivo* expression of PAX2 in the Fallopian tube mucosa

Cultured epithelial cells from the gynaecological tract, both in adults and at 20 weeks' gestation, were plated and colonies of clonogenic cells were characterized. The dominant immunophenotype associated with highly-proliferative clonogenic cell outgrowth was Krt7^p/PAX8^p/EZH2^p/ PAX2ⁿ/Krt5ⁿ/p63ⁿ (Figures 2A, 3A, and Supplementary Figure 2A). FOXJ1 expression indicating ciliated cell differentiation was also seen occasionally in the non-proliferative cells that were not stained positively with Ki67 (Figure 2A). To examine the differentiation ability of these cloned cells at the single-cell level, we established single-cell pedigree lines by subsequent rounds of plating and clone selection (Figure 2B). Pedigree lines of these cloned oviductal progenitor cells were differentiated

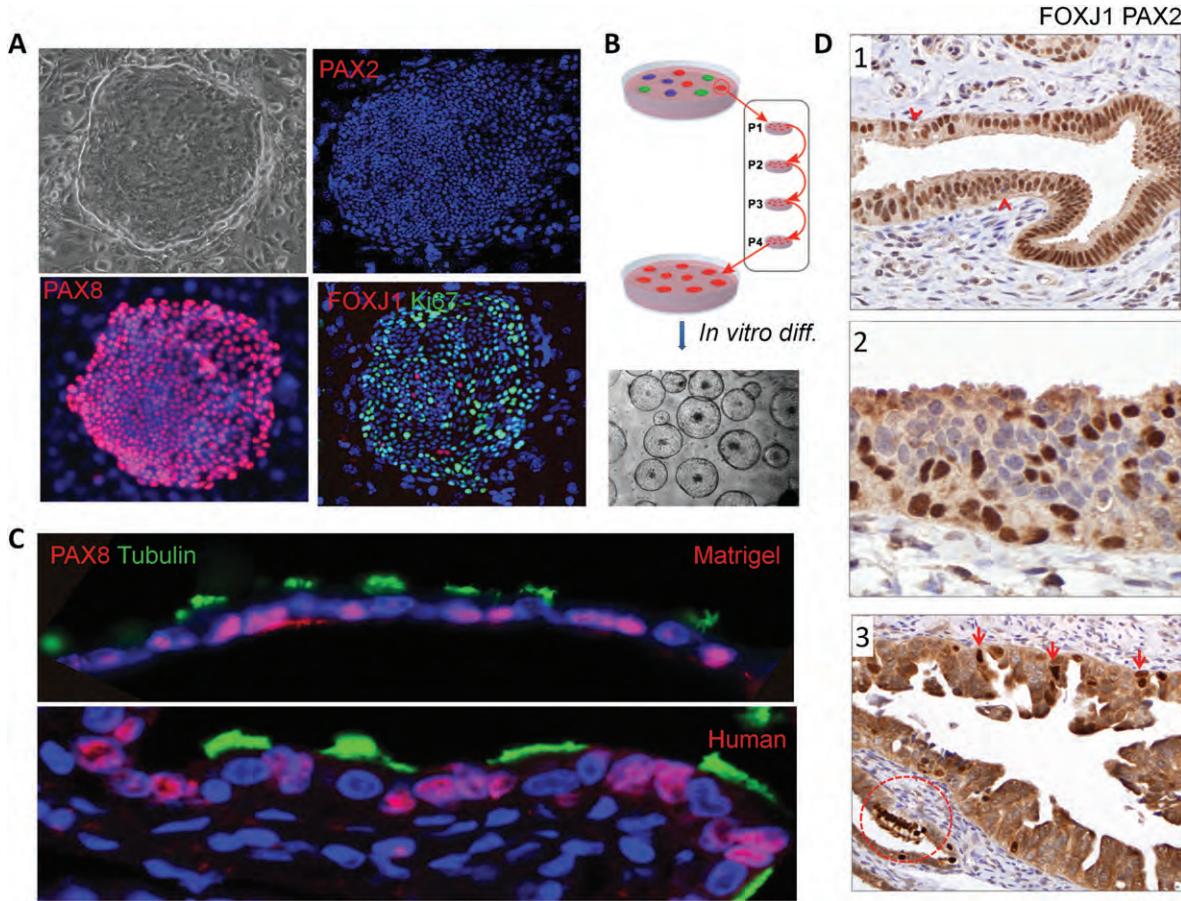
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Figure 2. *In vitro* propagation and differentiation of oviductal progenitor cells. (A) The cells cloned from fetal or adult oviduct are PAX2ⁿ, PAX8^p and occasionally express differentiation marker (FOXJ1) in non-proliferative cells (Ki67⁻). (B) Schematic diagram of pedigree cell line establishment. (C) Upper panel: representative image of fetal (20-week) oviductal progenitor cells differentiated in 3D Matrigel culture system. Lower panel: immunofluorescence image of human adult oviduct epithelium. Acetyl-alpha-tubulin (green) indicates ciliated cell differentiation. PAX8 (red) indicates non-ciliated cells. DAPI stains nuclei (blue). (D1) Combined staining of histological sections of normal tube with both PAX2 and FOXJ1 reveals widespread nuclear staining, except occasional lymphocytes (arrows). (D2) Occasional foci of multi-layered epithelium undergoing ciliated cell differentiation (positive nuclei) consist of some cells negative for PAX2. (D3) Tubal intraepithelial carcinoma with focal FOXJ1 staining (arrowheads) indicating ciliated cell differentiation. Circled focus of normal ciliated cells is an internal positive control.

in either an air–liquid interface (ALI) cell culture system or 3D Matrigel cultures for 10–20 days. In 3D Matrigel cultures, PAX8^p oviductal progenitor cells differentiated into columnar epithelium consisting of acetylated tubulin^p/FOXJ1^p/PAX8ⁿ ciliated cells and PAX8^p non-ciliated cells, which resembles the human oviduct histology (Figure 2C). In the ALI culture system, a series of images of acetylated tubulin expression were taken at different time points during the differentiation and showed that the oviductal progenitor cells started to differentiate into ciliated cells at day 3 and became maturely differentiated at day 10 (Supplementary Figure 2B). At day 10 in the ALI culture system, the cloned oviductal progenitor cells formed a simple epithelium with ciliated cells marked by FOXJ1 and acetylated tubulin and non-ciliated cells marked by PAX2 (Supplementary Figure 2C). It is noteworthy that while the proliferating population is PAX2ⁿ (Figure 2A), PAX2 expression was reclaimed in some non-ciliated (secretory) cells. This further indicates that the progeny of a single oviductal progenitor cell can

give rise to all epithelial lineages typically found in the oviduct, including not only mature ciliated cells but also non-ciliated (secretory) cells.

Immunostaining of both fetal and adult Fallopian tubes was performed to ascertain the distribution of PAX2-expressing cells and address the possibility that the PAX2ⁿ immunophenotype was programmed earlier in development. Histological sections of fetal (at 21 weeks) and adult Fallopian tubes were examined. Fetal tubes contained an abundance of PAX2^p cells, with occasional interspersed ciliated cells (Supplementary Figure 1A). Expression of PAX8 was similar in distribution (Supplementary Figure 1B). Similarly, in normal adult tubes, PAX2 staining was extensive in cells that were not undergoing ciliated (tubulin^p) differentiation (Supplementary Figure 1C). A summary of immunophenotypes for progenitor and adult cells is displayed in Supplementary Table 2.

In the adult tubes, sections were also stained with FOXJ1, and/or LCA to account for other PAX2ⁿ

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cells that were either undergoing ciliated differentiation or were non-epithelial. Mono-layered or mildly pseudostratified normal Fallopian tube mucosa typically contained cells expressing either PAX2 or FOXJ1 (Figure 2D1). In occasional foci of prominent multi-layered epithelium with some cells staining positive with FOXJ1, loss of PAX2 nuclear staining could be seen (Figure 2D2), giving the impression that loss of PAX2 expression in non-ciliated cells was coordinated with cell growth in multi-layered epithelium. Albeit less so, FOXJ1 staining was also seen in STINs, supporting ciliated differentiation in PAX2ⁿ neoplastic growth (Figure 2D3).

Metaplastic (WCNs) differentiation of PAX2ⁿ columnar cells *in vitro* and *in vivo*

WCNs are foci of transitional-like metaplasia in the fimbria or adjacent peritoneal surface and are emblematic of basal cell outgrowth that can develop near the junctions

of disparate epithelial types [19]. Other sites include the gastro-oesophageal and cervical squamo-columnar junctions. Both have been designated as sites harbouring residual embryonic cells and studies of the latter have suggested that basal or reserve cells emerge from the overlying columnar cells and then undergo squamous metaplasia [20,21]. This process has been termed 'top-down' differentiation, ie the progeny (basal cells) emerge from beneath the progenitor population. However, no study has ever displayed this sequence *in vitro*. Fetal tubal cells propagated *in vitro* were strongly positive for both Krt7 and PAX8, in keeping with Müllerian epithelium (Figures 2A and 3A). Moreover, these progenitor cells did not express Krt5 or p63 (Figure 3A). Interestingly, when pedigree lines of these cloned oviductal progenitor cells were differentiated in 3D Matrigel cultures for 10–20 days, in addition to the typical ciliated cell differentiation (Figure 2C), subjacent p63/Krt5^P basal cells emerged (Figure 3B1) and expanded (Figure 3B3) in a pattern similar to that

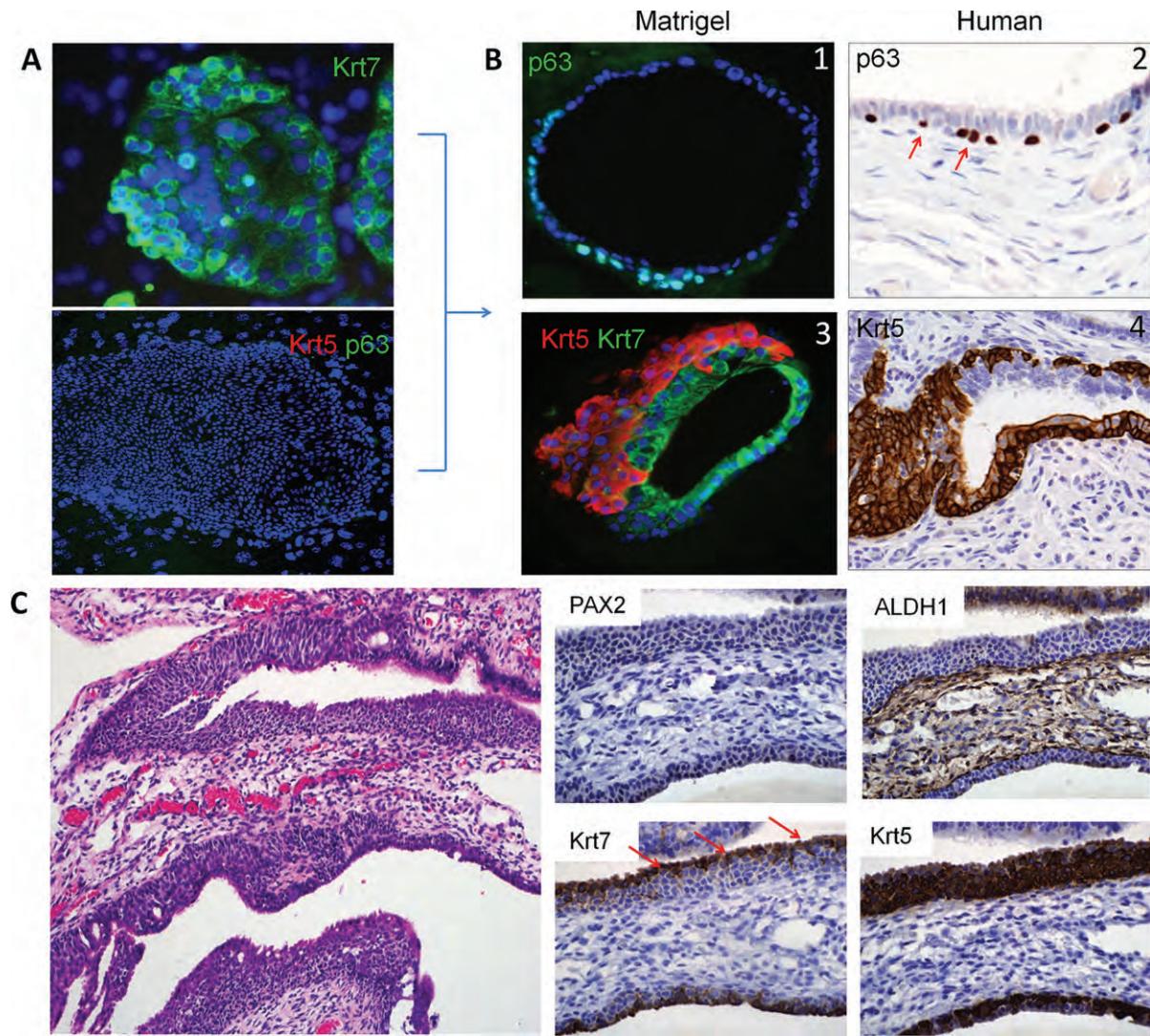


Figure 3. *In vitro* and *in vivo* basal cell differentiation in the oviduct. (A) Colonies of Krt7^P/Krt5ⁿ/p63ⁿ cells from a 20-week-old fetal oviduct. (B1, B3) Single (p63, green) and multi-layered (Krt5, red) basal cell outgrowth seen in Matrigel cultures. (B2, B4) Similar basal cell growth highlighted by p63 and Krt5 in the adult fimbria. (C) Walthard cell nest in the adult tube is typically PAX2 and ALDH1 negative. Residual Krt7-positive cells (arrows) are displaced from beneath by an expanding Krt5 population.

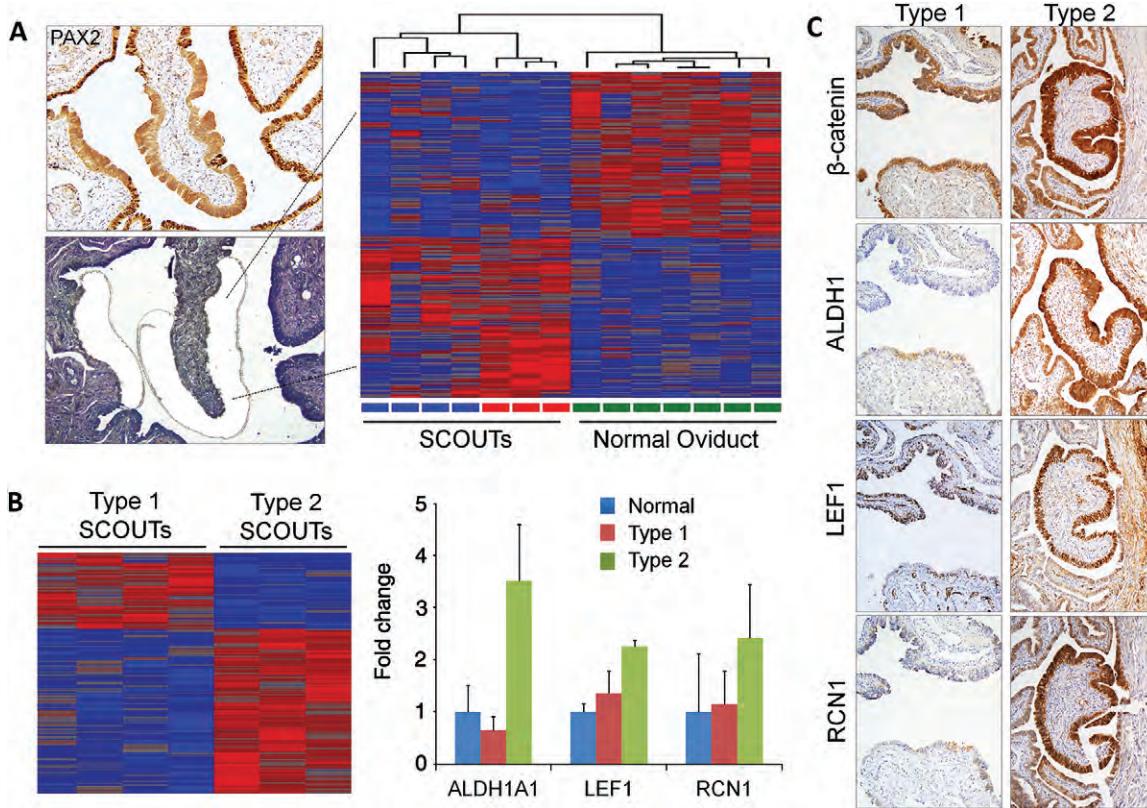
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Figure 4. (A) Laser-captured micro-dissected SCOUTs (left) and a heat map comparison of SCOUTs and normal oviduct (right). (B) Arrays generated from PAX2ⁿ SCOUTs revealed genes differentially expressed across type 1 and type 2 SCOUTs, including ALDH1, LEF1, and RCN1 (right). (C) Coordinated expression of the above genes distinguish type 1 SCOUTs, which show membranous β-catenin localization and absent ALDH1 staining plus negative or weak staining for LEF1 and RCN1 staining (left), from type 2 SCOUTs, with nuclear and cytoplasmic β-catenin, strong ALDH1, LEF1, and RCN1 staining (right).

seen in p63/Krt5^p cells in WCNs in the adult tube (Figures 3B2 and 3B4). *In vitro*, the Krt5 and p63 immunopositive cells were superimposed, although the Krt5 staining index was higher (Supplementary Figure 2E). Analysis of WCNs in tissue sections (Figure 3C) revealed a strikingly similar pattern of growth and differentiation, arising either from beneath Krt7^p epithelial cells or in continuity with columnar epithelium typical of type 1 SCOUTs. The result was a PAX2ⁿ/ALDH1ⁿ transitional-like outgrowth that was strongly Krt5^p but stathminⁿ (not shown). Taken in the context of the *in vitro* findings, this observation further linked the PAX2ⁿ immunophenotype to cell outgrowth and a Krt7^p progenitor cell to the development of not only terminal (FOXJ1⁺) but also metaplastic (Krt5⁺) differentiation in the Fallopian tube.

Altered gene expression in PAX2ⁿ proliferations (SCOUTs, STINs, and HGSCs)

Supplementary Table 3 is a list of genes selected for analysis and found to be differentially expressed in SCOUTs relative to normal-appearing epithelium. Arrays generated from RNA extracted from formalin-fixed laser-capture micro-dissected SCOUTs yielded differentially expressed genes, illustrated in the representative heat map (Figures 4A, 4B, and Supplementary Figures 4 and 5). When stained with selected

markers, type 1 SCOUTs varied from strictly secretory to mixed secretory and ciliated, and were ALDH1ⁿ, β-catenin^{mem} and stained weakly or negative for LEF1, RCN1, RUNX2, and EZH2 (Figures 4C, 5, and Supplementary Figure 3). Type 2 SCOUTs stained variably for ciliated cell differentiation and were β-catenin^{nc} and ALDH1, LEF1, RCN1, EZH2, RUNX2 (not shown) and stathmin positive (Figures 4C, 5, and Supplementary Figure 3). Basal cell differentiation, signifying WCN development, was associated with PAX2ⁿ columnar epithelium, suggesting that this pathway of differentiation might initiate within type 1 PAX2ⁿ SCOUTs.

Figure 5 and Supplementary Figure 6 summarize the staining patterns observed in the different lesions. STINs and HGSCs shared expression of several markers with SCOUTs. Expression patterns for ALDH and β-catenin were identical to type 1 SCOUTs (ALDHⁿ and β-catenin^{mem}). In addition, like type 2 SCOUTs, there was increased staining for EZH2, stathmin, LEF1, RCN, Krt5, and RUNX2 (not shown). Not surprisingly, no marker in this group separated STINs or HGSCs from SCOUTs. This is in contrast to other published markers such as Ki67, cyclin E, p16, and others, which are significantly more commonly expressed in STINs and HGSCs relative to benign Fallopian tube mucosa [4,5,15,22].

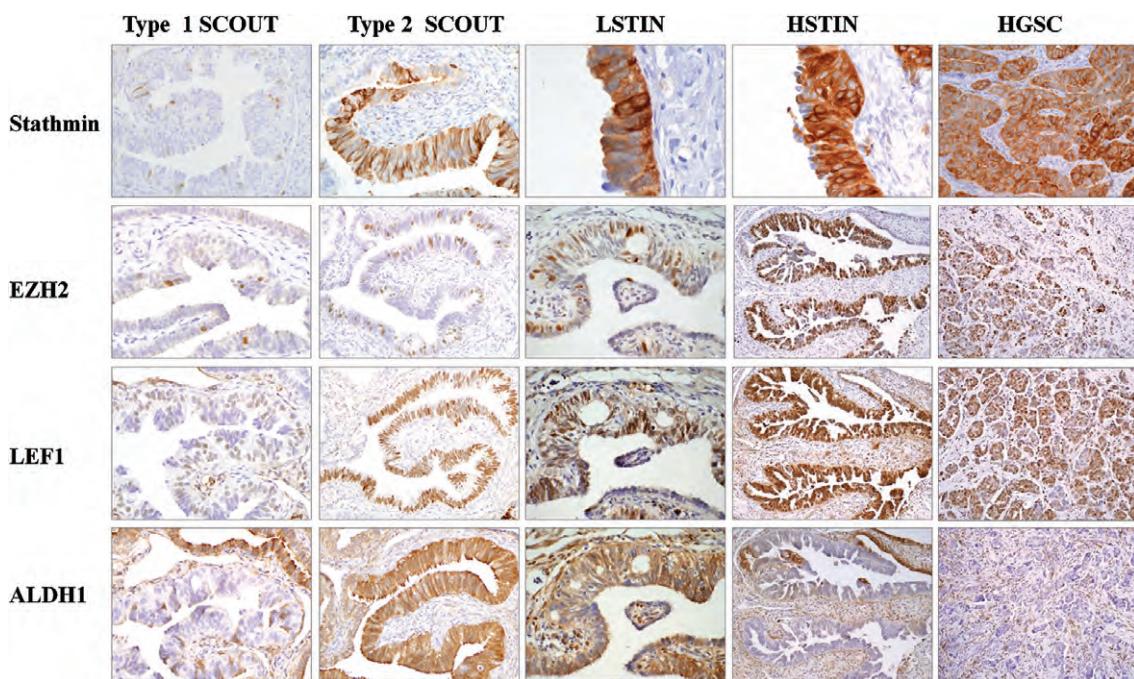


Figure 5. Shared expression of SCOUT markers with low- (LSTIN) and high- (HSTIN or STIC) grade serous tubal intraepithelial neoplasia and high-grade serous carcinoma (HGSC). Neoplasms (STINs, HGSCs) share with type 1 SCOUTs loss of PAX2 and ALDH1, and with type 2 SCOUTs, increased LEF1, EZH2, and other markers (see text).

Discussion

Analysis of arrays generated from high-grade serous cancer has confirmed a transcriptome that parallels oviductal epithelium [23]. Given that these tumours are strongly positive for biomarkers (such as PAX8) typically assigned to non-ciliated (so-called secretory) cells, the assumption has been that the secretory cell is the cell of origin [1]. Levanon *et al* showed that PAX8-expressing (secretory) cells of the tube were uniquely susceptible to DNA damage imposed by irradiation, a finding that parallels similar observations in latent precursors (p53 signatures) and STINs that contain p53 mutations [5,24]. However, with the discovery of PAX2ⁿ SCOUTs and a similar PAX2ⁿ expression pattern in many STINs, it became clear that there may be a relationship between the two entities, despite the fact that SCOUTs are more ubiquitous in the Fallopian tube and do not arise in the setting of a DNA damage response and loss of p53 function. Although altered PAX2 expression has been associated with neoplasia, we hypothesized that the PAX2ⁿ immunophenotype typified a 'generic' series of molecular events that were the underpinning of stem cell expansion common to many proliferations.

We addressed PAX2 expression or loss in the Fallopian tube from three perspectives. The first was by analysing expression and differentiation in proliferating normal adult and fetal cells propagated *in vitro*. The second was by comparing the *in vitro* findings to expression in tissue sections from fetal and adult tubes. The third was to look for shared expression across PAX2ⁿ cells in cell proliferation and expansion (SCOUTs,

STINs, and HGSCs). We discovered that the PAX2ⁿ immunophenotype was particularly linked to *in vitro* and *in vivo* cell growth, not infrequently with an increase in EZH2 expression. Moreover, in highly clonogenic Krt7^p/FOXJ1ⁿ oviductal progenitor cells grown *in vitro*, we demonstrated for the first time that PAX2ⁿ expanding populations were capable of both ciliated (FOXJ1) and basal cell (Krt5) differentiation. This sequence of cell growth and differentiation was recapitulated in SCOUTs, STINs, and HGSCs, with progressively reduced ciliated differentiation in the type 2 SCOUTs, STINs, and HGSCs. We thus concluded that all of these entities were related to a similar progenitor cell.

The next goal was to determine if the cells involved in benign and neoplastic outgrowth shared common expression patterns and we chose to use the least proliferative lesions (SCOUTs) as the reference. One advantage of this approach is to identify events that occur prior to the more dramatic molecular changes that characterize malignancy that may have profound influences on expression. The study delineated two general groups of SCOUTs: the first (type 1) closely resembled normal tubal epithelium, histologically and in their expression profile (Figure 1D). The second (type 2) was composed of proliferations with less pronounced ciliated differentiation, many noticeably 'endometrial'-like (Figure 1E). Accordingly, there was minimal difference in expression between type 1 SCOUTs and control epithelium, although they were consistently ALDH1ⁿ. In contrast, type 2 SCOUTs demonstrated nuclear and cytoplasmic β -catenin staining plus increased BCL2 (see ref 7), ALDH1, and Krt5 staining. This diversity in phenotype underscores the complexity of cell growth

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Progenitor cells in the Fallopian tube

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and differentiation that can occur in the Fallopian tubes with age. Type 1 SCOUTs appear to signify very minor genomic changes, as evidenced by the similarities in transcription to normal controls. Thus, the alterations in transcription are limited to absence of ALDH1 expression. In contrast, type 2 SCOUTs, which exhibit a more divergent histology, have a common biomarker signature – stathmin, EZH2, LEF1, RCN1, and RUNX2 – that is more similar to premalignant (STINs) and malignant (HGSCs) entities in the tube (Figure 5).

A fundamental question stemming from the above observation is the relevance of the gene signature found in SCOUTs, STINs, and HGSCs to both stem cell biology and neoplasia. ALDH1 has been identified as a marker of epithelial stem cells. Its expression can be both increased or absent, the latter more typical of STINs and HGSCs [25,26]. EZH2 is a polycomb suppressor that is implicated in stem cell maintenance and regulation of differentiation. It is noteworthy that EZH2 expression typically increased in areas of cell expansion, in keeping with the coordinated suppression of PAX2 expression [27]. EZH2 is also a potential suppressor of tumour suppressor genes [28]. LEF1 is likewise expressed during lineage differentiation [29]. The function of RCN1 is less clear but this gene product is a calcium binder that is weakly expressed in renal tubular cells and up-regulated in renal cell carcinomas [30]. RUNX2 is a gene involved in morphogenesis and osteoblastic differentiation [31]. Functions attributed to stathmin are multiple. It is a marker of P13 kinase

activation that has been linked to serous neoplasia in some studies, tumour progression and metastases in others, and regulates p53 stability in still others [32–34]. Its range of expression, including normal epithelium, SCOUTs, and STINs, is similar to that of these other markers, several of which (ALDH1, PAX2, EZH2) have also been linked to not only stem cells but also outcome or resistance to chemotherapy [35–37]. The significance of the unique β -catenin staining in type 2 SCOUTs, with a shift in distribution from the membrane to the cytoplasm and nucleus, is unclear but it is emblematic of Wnt pathway activation, and mutations in β -catenin are commonly found in endometrial and colon carcinomas [38].

Walthard cell nests are a common benign condition seen in the distal Fallopian tube mucosa or the adjacent peritoneal reflection [19]. They bear a close resemblance to the cervical squamo-columnar junction, where columnar cells are undermined by p63-positive basal cells. These cells could be envisioned to either originate from the columnar epithelium or give rise to the overlying Krt7-positive epithelial cells. This study has made two novel observations. First, based on the Matrigel cell culture data, the basal cells emerge from the Krt7-positive columnar cells. Second, this process is marked by not only loss of PAX2 but also ALDH1 expression, similar to that seen in type 1 SCOUTs. The initiating cell, the Krt7⁺ non-ciliated epithelial cell, is remarkably similar to the cells seen in the squamo-columnar (SC) junction of the cervix from which squamous metaplasia is derived and this process is similar to so-called ‘top-down’ differentiation reported in the SC junction [21]. The fact that

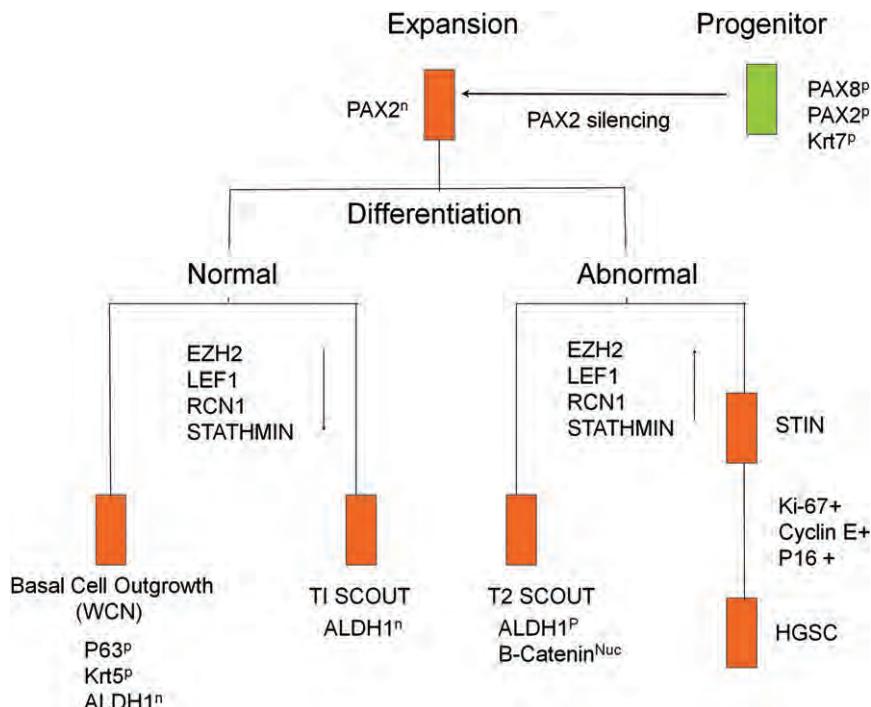


Figure 6. A progenitor cell model for the Fallopian tube in which Krt7 identifies the progenitor cell and PAX2ⁿ defines progenitor cell expansion. Expanding PAX2ⁿ cells can differentiate into basal or ciliated cells in WCNs or type 1 SCOUTs, both of which approximate normal differentiation pathways, with loss of ALDH1 and normal or minimally increased expression of LEF1, RCN1, stathmin, and EZH2. In contrast, type 2 SCOUTs and STINs (right) share a different expression signature characterized by multiple genes, including EZH2, LEF1, RCN1, and stathmin and others, involved in a divergent pathway of progenitor cell growth.

WCNs are not considered direct precursors to malignancy is not surprising, in as much as they are terminally differentiated relative to their progenitors. This is similar to the cervix, where the progenitor cells in the SC junction are considered more vulnerable to neoplastic transformation than their metaplastic progeny [21]. What is interesting is the fact that WCNs underscore the existence of multi-potential cells in the distal Fallopian tube [12]. Given that 40–60% of HGSCs do not have a documented source (or STIN) in the Fallopian tube mucosa, coupled with the fact that a subset of HGSCs are strongly Krt5-positive, the possibility that cells involved in alternate differentiation pathways might contribute to a subset of these malignancies deserves further study (Hanamornroongruang S, Howitt BE, Crum CP, unpublished) [5,25].

Epithelia in virtually every organ (breast being a prime example) display a wide range of clonal expansions, some of which may be direct precursors to malignancy and others of which serve as risk factors for a malignant outcome. The model depicted in Figure 6 reflects a similar but novel scenario in the oviduct, with multiple categories of putative monoclonal cell outgrowth and striking similarities in expression across multiple genes between surrogate precursors and lesions that are considered premalignant or pre-metastatic. These findings emphasize the complexity of molecular and phenotypic perturbations that can take place in the Fallopian tubes during and following menopause. This complexity invites caution when considering the role (or diagnostic value) of newly discovered biomarkers as specific indicators of neoplasia. More importantly, it reveals a consistent disturbance in progenitor cell biology in keeping with a common pathway that is triggered by more than one initiating event. Thus, it introduces two approaches to cancer prevention, one directed at the initiating event and the other at the early perturbations in the pathway.

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Author contribution statement

Contributions of the co-authors to design (1), data collection (2), data analysis (3), data interpretation (4), literature search (5), figures (6), and manuscript writing (7)

were as follows: GN (1–4, 6, 7); JGB (1–4, 6, 7); YY (1–3, 6); XW (2, 3); BEH (1, 2, 4, 5); MH (1–4); EY (1–3, 5); YH (2–4); MC (2–4); LW (2–4); SH (2–4); FDMcK (1, 4, 7); CPCr (1, 4, 7); and WX (1, 3, 4, 7).

Abbreviations

ALI, air–liquid interface culture; SCOUT, secretory cell outgrowth; STIN, serous tubal intraepithelial neoplasia; WCN, Walthard cell nest

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SUPPORTING INFORMATION ON THE INTERNET

The following supporting information may be found in the online version of this article:

Figure S1. Pax2 and acetyl-alpha-tubulin (cilia) expression in fetal and adult Fallopian tubes.

Figure S2. *In vitro* differentiation of oviduct progenitor cells.

Figure S3. Two types of PAX2^{hi} SCOUTs are distinguished in these panels with β -catenin, keratin 5, and LEF1 staining.

Figure S4. Heat map comparing type 1 and type 2 SCOUTs with normal tubal epithelium and high-grade serous cancer.

Figure S5. A depiction, in tabular (A) and graphical format (B), of genes up-regulated with the two-fold change in type 2 relative to type 1 SCOUTs, several of which have been linked to STIN and HGSC.

Figure S6. H&E, p53, and PAX2 staining of cases under study (see Figure 5).

Table S1. Biomarkers selected for analysis of clonogenic cells, SCOUTs, and STINs.

Table S2. Summary of immunophenotypes in cultured progenitor cells and adult cells in tissue sections.

Table S3. Upregulated genes in Type 2 SCOUTs in comparison with Type 1 SCOUTs (3 fold and $p < 0.05$).

Cloning and variation of ground state intestinal stem cells

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Stem cells of the gastrointestinal tract, pancreas, liver and other columnar epithelia collectively resist cloning in their elemental states. Here we demonstrate the cloning and propagation of highly clonogenic, ‘ground state’ stem cells of the human intestine and colon. We show that derived stem-cell pedigrees sustain limited copy number and sequence variation despite extensive serial passaging and display exquisitely precise, cell-autonomous commitment to epithelial differentiation consistent with their origins along the intestinal tract. This developmentally patterned and epigenetically maintained commitment of stem cells is likely to enforce the functional specificity of the adult intestinal tract. Using clonally derived colonic epithelia, we show that toxins A or B of the enteric pathogen *Clostridium difficile* recapitulate the salient features of pseudomembranous colitis. The stability of the epigenetic commitment programs of these stem cells, coupled with their unlimited replicative expansion and maintained clonogenicity, suggests certain advantages for their use in disease modelling and regenerative medicine.

While dominating prospective strategies for regenerative medicine, embryonic stem cells and induced pluripotent stem cells (iPSCs) face formidable challenges including risk of teratoma, complex guiding protocols for lineage specificity, and limited regenerative capacity of the lineages ultimately produced^{1–8}. The success and promise of iPSCs have largely overshadowed efforts to harness stem cells intrinsic to regenerative tissues. Green and colleagues developed methods for cloning epidermal stem cells⁹ that form a stratified epithelium upon engraftment, and these methods have been successfully applied to corneal, thymic and airway epithelia^{10–12}. However, stem cells of columnar epithelial tissues resist cloning in a manner that maintains their immaturity during proliferative expansion, and instead must be carried forward as regenerative, differentiating ‘organoids’^{13–18}. Despite their obvious potential in regenerative medicine and constant improvement¹⁹, the very low percentage of clonogenic cells in organoids limits the kinetics of their propagation as well as their utility for exploring the elemental stem cell.

The present study reports the cloning and propagation of ‘ground state’ human intestinal stem cells (ISC^{GS}). This technology offers insights into the molecular and functional features of columnar epithelial stem cells and their utility for disease modelling and regenerative medicine.

Cloning human fetal intestinal stem cells

We developed media (herein SCM-6F8) containing novel combinations of growth factors and regulators of TGF- β /BMP (transforming growth factor- β /bone morphogenetic protein), Wnt/ β -catenin, EGF (epidermal growth factor), IGF (insulin-like growth factor) and Notch

pathways^{9,20,21} that supports the maintenance of human intestinal stem cells in a highly clonogenic, ground state form. Thus single-cell suspensions of intestinal epithelia derived from 20- to 21-week-old fetal demise cases yield colonies comprised of highly immature cells in which differentiation markers can be induced by Notch suppression (Fig. 1a). Following induced differentiation via Wnt withdrawal, we were unable to recover ground state stem cells by our methods (Extended Data Fig. 1a–c).

The clonogenicity of cells in the colonies was determined by single-cell transfer to be greater than 50% (Fig. 1b). This high clonogenicity permits the rapid generation of single-cell ‘pedigree’ lines for expansion and characterization of lineage fates upon differentiation¹² (Fig. 1b). Pedigree lines of ISC^{GS} and tracheobronchial stem cells (TBSC^{GS})¹² grown for several months in culture were differentiated in air-liquid interface (ALI) cultures for 10–30 days (Fig. 1c). The ISC^{GS} formed a highly uniform, 3D serpentine pattern, whereas TBSC^{GS} produced a stratified epithelium with apically positioned ciliated and goblet cells. Histological sections of differentiated ISC^{GS} revealed a columnar epithelium of villus-like structures marked by goblet (Muc2⁺), endocrine (chromogranin A⁺), and Paneth cells and polarized villin expression (Fig. 1d; Extended Data Fig. 1d), indicating that the progeny of a single ISC^{GS} can give rise to all epithelial lineages typically found in the small intestine. Importantly, differentiation of these ground state stem cells is accomplished by exposure to an ALI rather than a removal of factors such as Wnt that maintain immaturity.

While principal component analysis (PCA) of differentially expressed genes of ground state stem cells and ALI-differentiated

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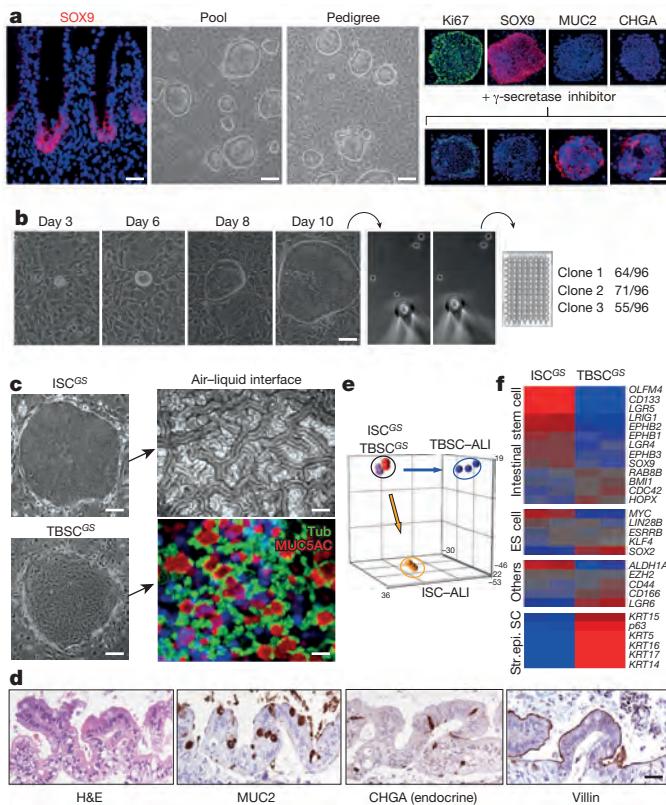


Figure 1 | Cloning stem cells from fetal intestine. **a**, Left, Sox9 expression in fetal intestine, scale bar, 25 μ m; colonies from intestine ($n = 10$ biological replicates; colonies of ISC pedigree ($n = 30$ independent experiments)). Scale bar, 75 μ m. Right, ISC colonies stained with indicated antibodies. $n = 4$ technical replicates. Bottom, marker expression following Notch inhibition. $n = 4$ technical replicates. **b**, Left, ISC colony growth. Scale bar, 75 μ m. Right, clonogenicity of colony cells. $n = 3$ biological replicates. **c**, ISC and TBSC pedigrees and ALI differentiation (tubulin, green; Muc5AC, red). Scale bar, 50 μ m left, 25 μ m right top, 25 μ m bottom right; $n = 7$ biological replicates; $n = 3$ technical replicates; 3 independent experiments. **d**, ALI-differentiated ISC. Scale bar, 50 μ m. $n = 7$ biological replicates; $n = 3$ technical replicates; 3 independent experiments. H&E, haematoxylin and eosin staining. **e**, PCA using 2,158 genes (> twofold, $P < 0.05$ by Student's *t*-test) of ISC and TBSC and corresponding ALI-differentiated epithelia. **f**, Expression heat map of markers in ISC and TBSC. Scale, -2.5-fold (extreme blue) to +2.5-fold (extreme red). $n = 3$ technical replicates.

tissue showed great divergence as expected for columnar and stratified epithelia, the gene expression profiles of undifferentiated ISC^{GS} and TBSC^{GS} differed by less than 4% (>2.0-fold, $P < 0.05$) (Fig. 1e). ISC^{GS} showed high expression of intestinal stem-cell markers such as OLFM4, CD133 (ref. 22), Lgr5 (ref. 23) and Lrig1 (ref. 24), whereas those from the airways had the typical stem cell markers of stratified epithelia (Krt14, Krt5 and Tp63 (ref. 11)) (Fig. 1f).

Intestinal stem cell variation

Approximately one in 2,000 cells from duodenum (I^{du}SC), jejunum (I^{je}SC) and ileum (I^{il}SC) of a 21-week-old fetal intestine form a colony (Fig. 2a). Although these colonies were morphologically indistinguishable in culture, whole-genome expression analysis of multiple pedigrees showed a consistent, region-specific signature of 24–178 genes (>1.5-fold, $P < 0.05$; Fig. 2b; Extended Data Fig. 2a).

After 10 days at an ALI, I^{du}SC and I^{je}SC gave rise to a finer pattern of epithelial folds than that produced by I^{il}SC (Fig. 2c). By histology, villi appear progressively more robust along the anterior–posterior axis, with I^{il}SC producing the larger villi and more numerous goblet cells (Fig. 2d, e). Interestingly, the epithelia derived from I^{du}SC expressed markers more typical of gastric epithelium (for example,

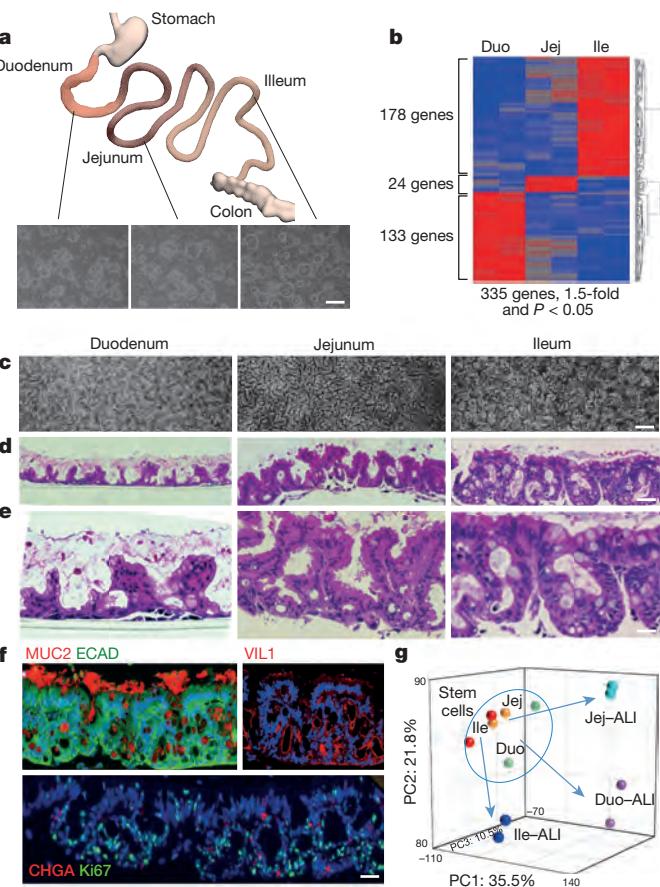


Figure 2 | Stem cells from fetal small intestine. **a**, Depiction of small intestine and clones derived from each. Scale bar, 400 μ m; $n = 3$ biological replicates. **b**, Heat map of pedigrees from duodenum (Duo), jejunum (Jej), and ileum (Ile). **c**, Surface views of ALI cultures. Scale bar, 200 μ m; $n = 30$ technical replicates. **d**, **e**, Histological sections through ALI cultures at low (scale bar, 150 μ m) and high (scale bar, 50 μ m) magnification. **f**, Immunofluorescence on sections of ALI cultures with indicated antibodies. ECAD, E-cadherin. Scale bar, 75 μ m; $n = 3$ technical replicates. **g**, PCA map of stem cell gene expression from the three major regions of the small intestine together with their corresponding ALI-differentiated epithelia.

TFF2 and Muc5AC), consistent with duodenum's location between the stomach and the small intestine (Extended Data Fig. 2b). I^{je}SC-derived epithelium, however, expressed Muc2, consistent with intestinal epithelium (Extended Data Fig. 2c), and I^{il}SC produced an epithelium more akin to colon (Fig. 2f). The pattern of proliferation in the ALI epithelia as measured by Ki67 staining was generally confined to cells proximal to the support membrane (Fig. 2e, f). PCA mapping of gene expression revealed more divergence among ALI-differentiated tissue than among the intestinal stem cells (Fig. 2g).

Colon stem cells

We also generated single-cell pedigree lines from the ascending, transverse, and descending colon from the same 21-week fetal demise case (Fig. 3a). The variation in gene expression between the stem cells of these colonic segments was minimal with signatures of 19–28 genes (>1.5-fold, $P < 0.05$; Fig. 3b). As with pedigrees derived from the intestinal epithelium, those from the colon could be propagated for months without loss of clonogenicity (not shown). Differentiation of these colon pedigrees under identical ALI conditions employed for the intestinal stem cells resulted in networks of 3D, large-diameter structures (Fig. 3c). Consistently, the histology of these ALI cultures revealed patterns of broad intestinal glands dominated by goblet cells (Fig. 3d). These ALI-generated tissues showed strong staining for

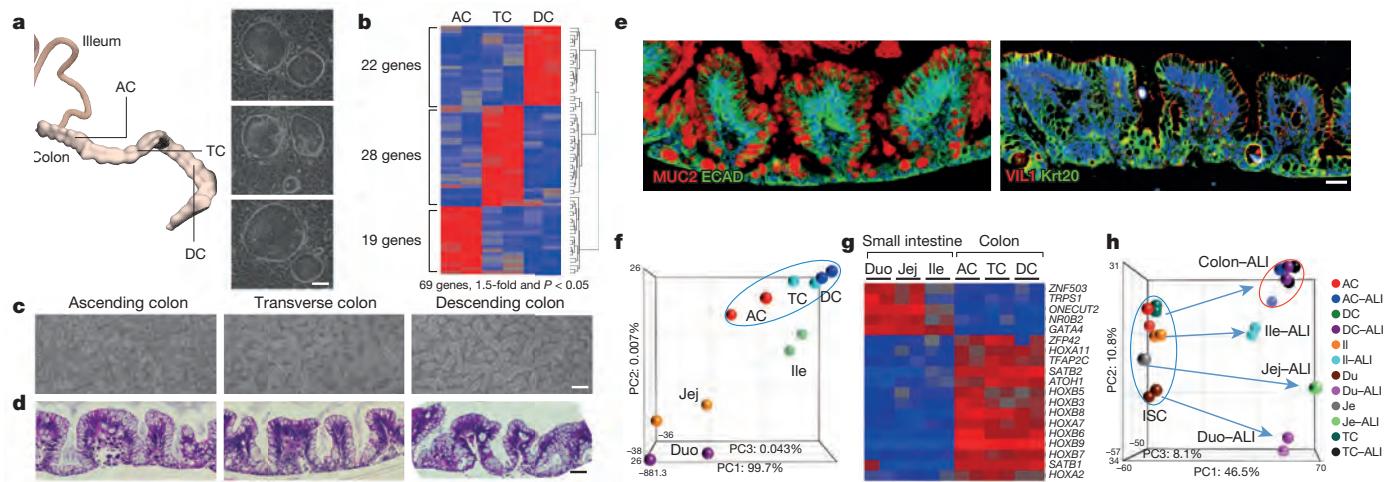


Figure 3 | Stem cells of fetal colon. **a**, Depiction of colon and clones derived from each. Scale bar, 75 μ m; $n = 3$ biological replicates. AC, TC and DC, ascending, transverse and descending colon, respectively. **b**, Expression heat map of pedigrees from the three major divisions of the colon. **c**, Surface images of ALI cultures. Scale bar, 100 μ m; $n = 20$ technical replicates. **d**, Histological sections through ALI cultures of colon stem cells. Scale bar, 75 μ m. **e**, Immunofluorescence on sections through ALI cultures with indicated antibodies. Scale bar, 50 μ m. **f**, PCA map of gene expression of colon and intestine stem cells. **g**, Expression heat map of stem cells of small intestine and colon. **h**, PCA map of gene expression profiles of intestinal stem cells and their corresponding ALI-differentiated epithelia.

intestinal goblet cell marker Muc2, as well as polarized villin and Krt20, typical of differentiated colonic epithelium (Fig. 3e). And while the colonic stem cells as a group showed minor differences in gene expression (see Figure 3b), they gave rise to epithelia with more distinct gene expression profiles (Extended Data Fig. 3). PCA mapping of these expression data showed a clustering of the colon stem cells relative to the intestinal stem cells, with increasingly distant spaces occupied by stem cells of the ileum, jejunum and duodenum, respectively (Fig. 3f). This distinction in global gene expression patterns is reflected, for instance, in the differential expression of transcription factors. In particular, *ONECUT2*, *NR0B2*, *TRPS1* and *ZNF503* show relatively high expression in the small intestine stem cells, whereas those of the colon showed a bias for *Hox* genes as well as the global chromatin organizer genes *SATB1* and *SATB2* (Fig. 3g, h).

Columnar versus stratified epithelia

The expression profiles of stem cells of human intestinal tract enabled a detailed comparison with those of stratified epithelia including human epidermis, corneal epithelium, mammary gland, prostate gland and upper airway. From this analysis it is clear that stratified epithelia, all of which depend on the p53-related stem-cell marker p63 for long-term self-renewal¹¹, occupy a distinct expression space from that of the intestinal stem cells or other columnar epithelial stem cells (Fig. 4a). A survey of genes whose expression is associated with stem cells of one of these two major classes of epithelia revealed a strong bias for *Olfm4*, *CD133* (ref. 22), *Lgr5* (ref. 23), *Nr5a2* (ref. 25), *Id2*, *Lrig1* (ref. 24), *EphB2*, *Ascl2* and *EphB3* in the intestinal stem cells, while the stratified epithelial stem cells expressed *ZNF750*, *TP63* and *KRT5* (Fig. 4b). Many of the markers differentially appearing in the intestinal stem cells, such as *Olfm4*, *Lgr5* and *Ascl2*, are not general

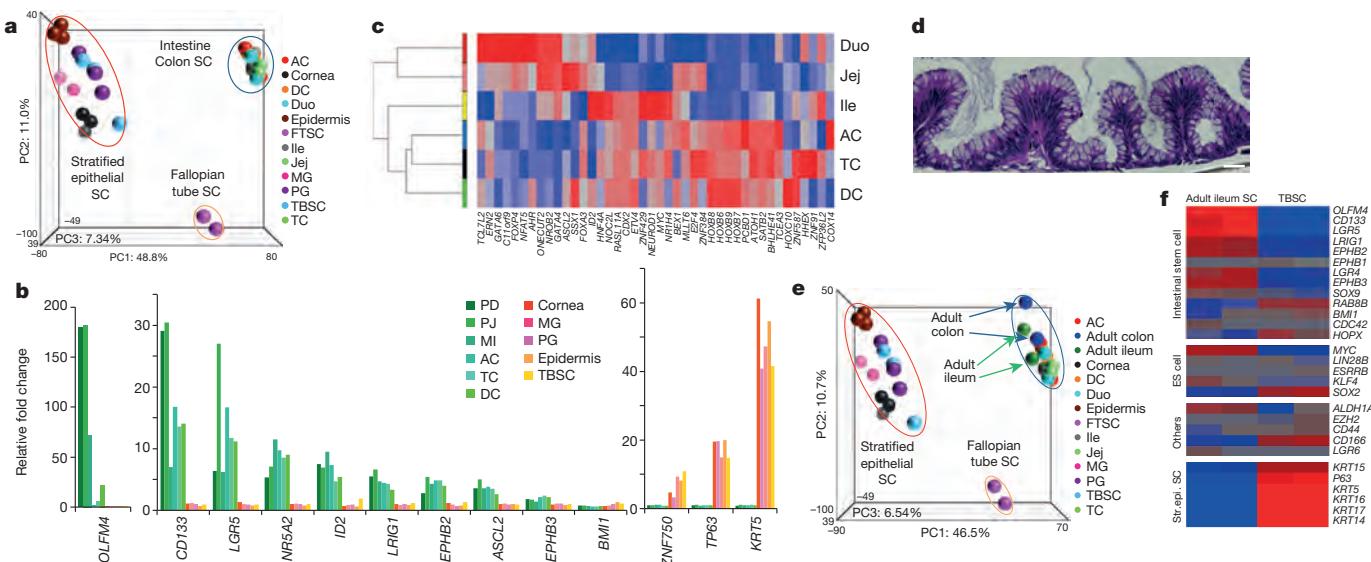


Figure 4 | Differential gene expression in stem cells of stratified and columnar epithelia. **a**, PCA map of stem cells of stratified epithelia (cornea, corneal epithelium; MG, mammary gland; PG, prostate gland; TBSC, tracheo-bronchial epithelial stem cells) and columnar epithelia (FTSC, fallopian tube epithelium). **b**, Gene expression in stem cells (stratified epithelia $n = 3$ technical replicates; columnar epithelia $n = 2$ technical replicates). **c**, Transcription

factors differentially expressed in TBSC and ISC. **d**, ALI-differentiated adult terminal ileum stem cells derived from endoscopic biopsy. Scale bar, 50 μ m; $n = 10$ technical replicates. **e**, PCA map of stem cells of adult terminal ileum, colon, fetal ISCs, and stratified epithelia. **f**, Stem cell markers in adult terminal ileum stem cells and TBSCs.

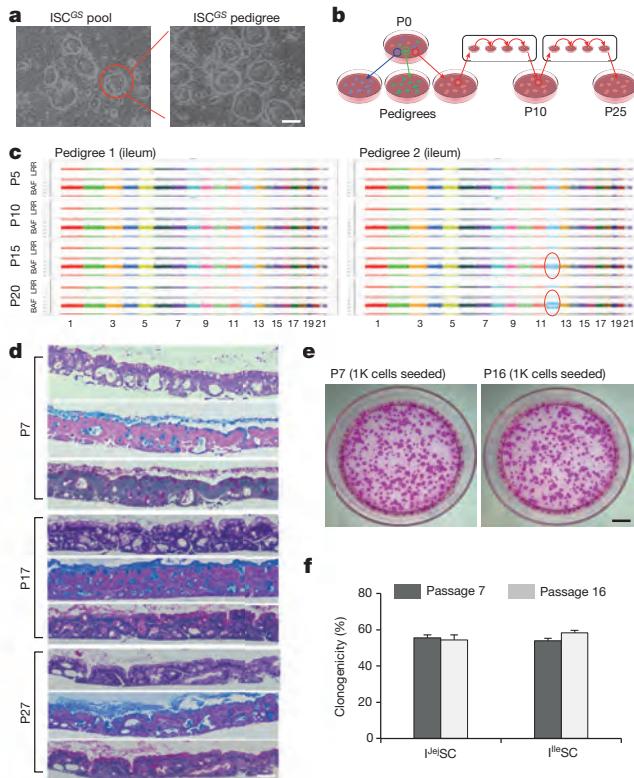


Figure 5 | Genomic stability of ISC in culture. **a**, Clone selection for pedigree generation. Scale bar, 200 μ m. **b**, Serial passaging of pedigrees. **c**, CNV, BAF (B allele frequency) and LRR (log R ratio) profiles of pedigrees at P5 to P20 and trisomy 12 indicated (circle). **d**, ALI-differentiated pedigree 2 at P7, P17, and P27 stained with H&E (top), Alcian blue (middle), and periodic acid Schiff (bottom). Scale bar, 100 μ m; $n = 4$ technical replicates. **e**, Clonogenicity assay revealing Rhodamine red-stained colonies grown 20 days following seeding 1,000 passaged cells. Scale bar, 10mm; $n = 3$ technical replicates. **f**, Quantification of clonogenicity at indicated passage number of ground state stem cells from jejunum (JeSC) and ileum (IleSC). $n = 3$ biological replicates; error bars, s.d.

columnar epithelial stem cell markers as evidenced by their absence in fallopian tube stem cells, although Lrig1 is more highly expressed in fallopian tube stem cells than either those of the intestine or the colon (Extended Data Fig. 4a). Notably, Bmi1, a member of the Polycomb group (PcG) PRC1-like complex implicated in self-renewal in both haematopoietic²⁶ and as reserve cells for proliferating, Lgr5⁺ intestinal stem cells^{27–29}, was not differentially expressed in the cloned intestinal versus stratified epithelial stem cells. And while many of the typical markers of intestinal stem cells such as Lgr5, CD44, Lrig1, EphB2 and ASCL2 show a decrease in expression as the intestinal stem cells are differentiated in ALI cultures, Bmi1 did not (Extended Data Fig. 4b, c). These findings suggest that we are cloning either crypt cells or so-called ‘+4’ cells that have become crypt-like in their expression patterns. We also examined transcription factors differentially expressed in ISC compared to stratified epithelial stem cells in an effort to understand the regiospecificity of commitment programs of stem cells along the intestinal tract (Fig. 4c). In addition to six transcription factors that were uniformly highly expressed in stem cells of the intestinal tract (CREB3L1, Myb, NR5A2, IRF8, HNF4G and Msx2) versus tracheobronchial stem cells, this analysis revealed limited sets of transcription factors differentially expressed in stem cells along the anterior–posterior axis of the intestinal tract that conceivably function in maintaining commitment states. For instance, and consistent with previous observations³⁰, GATA4 and GATA6 were expressed most strongly in the anterior portions of the intestinal tract (Fig. 4c). Significantly, the selective deletion of GATA4

and GATA6 in the murine duodenum and jejunum promotes ileal properties and a detrimental phenotype^{30,31}, suggesting a role for these transcription factors in maintaining segmental identity acting at the level of the stem cell. Similarly, the requirement for Onecut2 in the duodenum³² might be at the level of the duodenal stem cells. It is likely that analyses of cloned stem cells from the various segments of the intestinal tract will help to unravel the roles of such segment-specific transcription factors in the establishment of commitment and differentiation programs. Importantly, the overall properties of ISCs from fetal sources are conserved in those derived from endoscopic biopsies of paediatric and adult cases (Fig. 4d–f).

Genomic and lineage stability

Human embryonic stem cells and iPSC lines acquire with successive passages genomic structural variations, including some that confer a selective advantage^{33,34}. To assess the genomic stability of our ISC^{GS}, we examined copy number (CNV) and single nucleotide variation (SNV) in two independent ISC^{GS} pedigrees derived from the ileum of one fetal demise case after 50 (passage 5; P5), 100 (P10), 150 (P15), and 200 days (P20) of continuous proliferation (Fig. 5a, b). At P5, when single ISC^{GS} pedigrees can be amplified to an estimated 300 million to 75 billion cells, no chromosomal aneuploidies were detected, although one pedigree showed three interstitial deletions affecting two genes (Fig. 5c; Extended Data Fig. 5a; Supplementary Information Table 1). This low level of structural variation was maintained through passage 10, although increased by P15 and at P20 one of the pedigrees showed a frank trisomy of chromosome 12 (Fig. 5c; Extended Data Fig. 5a; Supplementary Information Table 1). A similar upward trend in CNV as a function of passage number was observed in five intestinal pedigrees (pedigrees 3–7) derived from a separate fetal demise case (Extended Data Figs 5, 6; Supplementary Information Tables 1, 2).

By exome sequencing, our original two pedigrees showed few (0–1) non-synonymous mutations through passage 10, and these increased modestly (1–2 new non-synonymous mutations) through P15 and P20 (Extended Data Fig. 5a). None of these non-synonymous mutations have been reported as driver genes in human cancers. A similar trend was observed in the five pedigrees from the second fetal demise case followed through P5 and P25. By P25 the range of non-synonymous SNVs increased to 2–10 per clone, and while not involving obvious cancer driver genes, did include genes such as *ECT2L* and *EP300* that might provide a selective growth advantage (Extended Data Fig. 5c). These data indicate that most pedigrees sustain few genomic changes within the first 100 days of proliferative expansion. By P15 and through P25, however, half the pedigrees showed evidence for aneuploidy as well as an increase in interstitial CNV and SNVs with allele frequencies nearing 0.5, suggesting the rise of an advantaged subclone. We asked how these late-passage genomic changes might affect differentiation by comparing early and late passages of pedigree 2 in ALI differentiation. By all histological criteria, including Alcian blue staining for goblet cells and intestinal marker staining, we could not distinguish the ALI-differentiated epithelia derived from P7, P17 and P27 (Fig. 5d; Extended Data Fig. 7). Similarly, we note that these intestinal stem cell pedigrees do not lose (or gain) clonogenicity when tested at P7 and P16, which remain stably above 50% (Fig. 5e, f). Lastly, we found no evidence of tumorigenicity by these ground state intestinal stem cells, including those at P25 harbouring aneuploidies, following their subcutaneous implantation to immunodeficient (NOD.Cg-Prkdc^{scid} Il2rg^{tm1Wjl}/SzJ) mice³⁵ (Extended Data Fig. 8).

Modelling *Clostridium difficile* infections

C. difficile is a Gram-positive, spore-forming bacterium and the primary cause of nosocomial diarrhoea and pseudomembranous colitis³⁶. The pathogenicity of *C. difficile* is linked to its production of two similar, high molecular weight toxins TcdA and TcdB. While together TcdA and TcdB cause fluid secretion, inflammation, and colonic

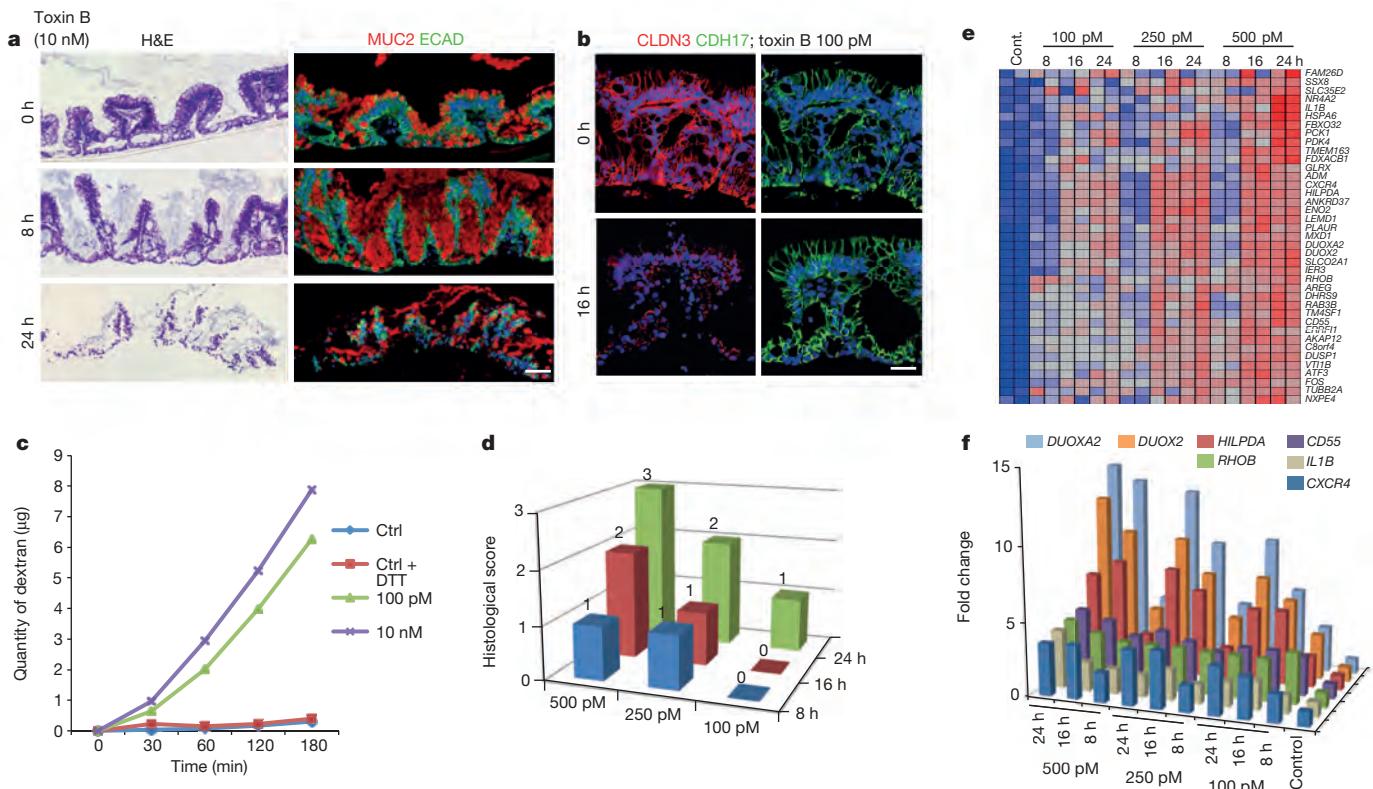


Figure 6 | *C. difficile* toxin B effects on *in vitro*-generated colonic epithelia. **a**, TcdB effects on colonic stem cell-derived epithelia. Scale bar, 100 μ m; $n = 4$ technical replicates. **b**, Tight junction protein claudin 3 (CLDN3; red) and adherens junction marker cadherin-17 (CDH17; green) in ALI colonic epithelium treated with TcdB. Scale bar, 50 μ m; $n = 4$ biological replicates. **c**, Dextran permeability assay on TcdB-treated ALI colonic epithelia. **d**, 3D plot

of histological scoring by gastrointestinal pathologist according to a standard 0–3 rating for colonic epithelial integrity. **e**, Heat map of 39 genes differentially expressed between TcdB (500 pM, 24 h) and controls (>3 fold and $P < 0.05$ by Student's *t*-test). **f**, 3D plot of seven selected genes at time points and doses indicated. $n = 2$ technical replicates.

tissue damage, their respective and possible synergistic roles have been difficult to ascertain^{37–39}. We therefore challenged colonic epithelia derived from cloned, ground state colonic stem cells with recombinant TcdB (Fig. 6a, b; Extended Data Fig. 9a, b). At higher concentrations or longer time points there is a loss of goblet cells, disruption of the crypt architecture, cell polarity, and a specific loss of tight versus adherens junction proteins that correlates with increased dextran permeability (Fig. 6c). These dose–response changes in the ALI colonic epithelium mirror those of *C. difficile*-associated pseudo-membranous colitis (Fig. 6d, Extended Data Fig. 9a, b). Microarray analysis of ALI-generated colonic epithelia following nine TcdB treatment conditions revealed alterations in gene expression in a time- and dose-dependent manner (Fig. 6e, f; Extended Data Fig. 9c–f). Pathway analysis indicated that TcdB triggers changes in gene expression related to inflammation, RhoB-mediated actin regulation, and junctional dynamics previously implicated in *C. difficile* pathology^{40,41}. In addition, this analysis revealed that DUOX2 and DUOXA2 were consistently the two highest upregulated genes (Fig. 6e, f). These proteins form an enzyme capable of producing hydrogen peroxide and have been implicated in the inflammation of inflammatory bowel disease (IBD)⁴². Finally, we also tested *C. difficile* TcdA in our model. TcdA is reported to be a specific enterotoxin^{36,37}, and indeed we found that it triggers similar cytopathic and permeability changes in ALI models of human colonic epithelium (Extended Data Fig. 10), albeit at lower doses than those effective for TcdB. Together these findings underscore the potential of this model system to recapitulate and elucidate *C. difficile* pathology.

Discussion

Adult stem cells of the highly regenerative intestinal tract remain largely defined by metabolic, marker profiling, or lineage tracing

experiments *in vivo* or transplantation of cells from intestinal organoids^{23,43,44}. As stem cells comprise only a minor component of organoids—perhaps less than 1%⁴⁵—the molecular features of stem cells of columnar epithelia such as the intestinal tract have remained unclear. Therefore the selective cloning and proliferative expansion of highly clonogenic, ground state intestinal stem cells described here offers a first glimpse into the molecular properties of these cells. Our inability to convert differentiated cells to clonogenic cells supports the notion that we are cloning resident stem cells rather than somehow ‘reprogramming’ differentiated enterocytes. These resident stem cells possess robust epigenetic programs of commitment to regiospecific intestinal differentiation that are stable despite more than six months of continuous propagation. This cell-autonomous regiospecificity of stem cells along the intestinal tract argues against a unitary ‘intestinal stem cell’ or even one each for the histologically recognized segments, but rather a developmentally established spectrum of stem cells that ultimately maintains the histological and functional properties that define these segments. A heuristic deciphering of the commitment code from the regiospecific expression patterns presented here will guide parallel efforts with iPSCs to achieve appropriate lineage fates⁴⁶. Interestingly, many inductive signalling pathways and transcription factors implicated in embryonic gut formation⁴⁷ may act to reinforce commitment codes via continued expression in stem cells of the intestinal tract.

We anticipate that the ability to maintain these stem cells in their elemental state will enable the discovery of epigenetic mechanisms that underlie properties of very long-term self-renewal, exquisitely precise lineage commitment, and the intrinsically directed, self-assembly of differentiated epithelia. Although we demonstrate the potential of clonally-derived colonic epithelia to model the pathogenesis of *C. difficile* toxins, we anticipate the need to restore complexity

in the form of mesenchyme, immune cells, enteric neurons and perhaps components of the microbiome⁴⁸ to fully recapitulate disease dynamics. In particular, enteric maladies such as inflammatory bowel disease represent important medical challenges whose aetiologies most likely reside in interactions between the immune system, intestinal mucosa and intestinal flora^{49,50}. Finally, the ability to clone patient-specific, ground state stem cells from columnar epithelia via endoscopic biopsies, coupled with their orders-of-magnitude expansion kinetics over organoids, favours their use in regenerative medicine, pre-clinical trials and disease modelling.

Online Content Methods, along with any additional Extended Data display items and Source Data, are available in the online version of the paper; references unique to these sections appear only in the online paper.

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Author Contributions Experimental design and conception were done by W.X., F.M., D.B.L., K.Y.H. and C.P.C.; X.W. cloned and differentiated the intestinal stem cells with help from L.H.W., F.K., G.N., B.E.H. and Y.H.; Y.Y., X.W. prepared the genomic and gene expression analyses together with F.K., G.N., C.C.K. and L.W.; T.Z., D.B. and N.N. performed all computational and bioinformatics work. B.H. and C.P.C. obtained fetal tissues and F.A.S., J.S.H. and T.D. provided endoscopic biopsies, and R.B. analysed the xenografts. The *C. difficile* experiments were designed and executed by B.C., L.H.W., M.A.F. and D.B.L.; W.X. and F.M. wrote the manuscript with input from all other authors.

Author Information Data sets generated for this study have been submitted to the National Center for Biotechnology Information Gene Expression Omnibus (GEO) database and the European Nucleotide Archive under accession numbers GSE66749 and SRP056402. Reprints and permissions information is available at www.nature.com/reprints. The authors declare no competing financial interests. Readers are welcome to comment on the online version of the paper. Correspondence and requests for materials should be addressed to W.X. (xianmckeon2014@gmail.com) or F.M. (mckeon.xian@gmail.com).

METHODS

In vitro culture of human small intestinal and colonic epithelial stem cells.

Intestinal tissue from 20- to 21-week-old late fetal demise cases were obtained under parent consent as de-identified material under approved institutional review board protocols at the Brigham and Women's Hospital, Boston, MA, USA (2009P002281). Terminal ileum endoscopic biopsies were obtained under informed consent and institutional review board approval at the Connecticut Children's Medical Center, Hartford, Connecticut USA (15-047J-2). Fetal intestinal tissue or 1 mm endoscopic biopsies from terminal ileum were collected into cold F12 media (Gibco, USA) with 5% fetal bovine serum (HyClone, USA) and then minced by sterile scalpel into 0.2–0.5 mm³ sizes to a viscous and homogeneous appearance. The minced tissue was digested in 2 mg ml⁻¹ collagenase type IV (Gibco, USA) at 37 °C for 30–60 min with agitation. Dissociated cells were passed through a 70-μm Nylon mesh (Falcon, USA) to remove aggregates and then were washed four times in cold F12 media, and then seeded onto a feeder layer of lethally irradiated 3T3-J2 cells^{9,12} in c-FAD media⁹ modified to SCM-6F8 media by the addition of 125 ng ml⁻¹ R-spondin1 (R&D systems, USA), 1 μM Jagged-1 (AnaSpec Inc., USA), 100 ng ml⁻¹ human Noggin (Peprotech, USA), 2.5 μM Rock-inhibitor (Calbiochem, USA), 2 μM SB431542 (Cayman chemical, USA), and 10 mM nicotinamide (Sigma-Aldrich, USA). Cells were cultured at 37 °C in a 7.5% CO₂ incubator. The culture media was replaced every two days. Colonies were digested by 0.25% trypsin-EDTA solution (Gibco, USA) for 5–8 min and passaged every 7 to 10 days. To obtain single-cell suspensions colonies were trypsinized by TrypLE Express solution (Gibco, USA) for 8–15 min at 37 °C and cell suspensions were passed through 30-μm filters (Miltenyi Biotec, Germany). Approximately 20,000 epithelial cells were seeded to each well of 6-well plate. Cloning cylinder (Pyrex, USA) and high vacuum grease (Dow Corning, USA) were used to select single colonies for pedigrees. Gene expression analyses were performed on cells derived from passage 4–8 (P4–P8) cultures.

Histology and immunostaining. Histology, haematoxylin and eosin (H&E), Alcian blue, periodic acid-Schiff (PAS), rhodamine B staining, immunohistochemistry, and immunofluorescence were performed using standard techniques. For immunofluorescence and immunohistochemistry, 4% paraformaldehyde fixed, paraffin-embedded tissue sections were subjected to antigen retrieval in citrate buffer (pH 6.0, Sigma-Aldrich, USA) at 120 °C for 20 min, and a blocking procedure was performed with 5% bovine serum albumin (BSA, Sigma-Aldrich, USA) and 0.05% Triton X-100 (Sigma-Aldrich, USA) in phosphate-buffered saline (PBS; Gibco, USA) at room temperature for 1 h. Primary antibodies used in this study and staining condition were listed in Supplementary Information Table 3. All images were captured by using the Inverted Eclipse Ti-Series (Nikon, Japan) microscope with Lumencor SOLA light engine and Andor Technology Clara Interline CCD camera and NIS-Elements Advanced Research v.4.13 software (Nikon, Japan) or LSM 780 confocal microscope (Carl Zeiss, Germany) with LSM software. Bright field cell culture images were obtained on an Eclipse TS100 microscope (Nikon, Japan) with Digital Sight DSFi1camera (Nikon, Japan) and NIS-Elements F3.0 software (Nikon, Japan).

Stem cell differentiation. Air-liquid interface (ALI) culture of TBSCs was performed as described^{12,51}. Briefly, for ALI culture of intestinal and colonic epithelial stem cells, Transwell inserts (Corning, USA) were coated with 20% Matrigel (BD Biosciences, USA) and incubated at 37 °C for 30 min to polymerize. 200,000 irradiated 3T3-J2 cells were seeded to each transwell insert and incubated at 37 °C, 7.5% CO₂ incubator overnight. QuadroMACS Starting Kit (LS) (Miltenyi Biotec, Germany) was used to purify the stem cells by removal of feeder cells. 200,000–300,000 stem cells were seeded into each Transwell insert and cultured with SCM-6F8. At confluence (3–7 days), the apical media was removed through careful pipetting and the cultures were continued for an additional 6–12 days before analysis.

Clostridium difficile toxin treatment and epithelial permeability assay.

Clostridium difficile toxins A and B (TcdA, TcdB) were prepared as described⁵². Intestinal stem cells were differentiated in air-liquid interface cultures as described above and treated with 100, 250, 500 pM and 10 nM TcdA or TcdB for 0, 8, 16, and 24 h. At these time points, membranes with differentiated epithelia were collected for histology and microarray analysis. 4 kDa FITC-dextran (Sigma-Aldrich, USA) was added to the apical chamber of the Transwell chambers for a final concentration of 0.5 mg ml⁻¹. Media was removed from the bottom compartment after different incubation times and fluorescence was read by fluorometer (Infinite M1000 PRO, excitation 490 nm, emission 520 nm, Tecan, USA).

Implantation of intestinal stem cells. Intestinal stem cells (1.5 million cells) from different pedigrees with 50% of Matrigel (BD Bioscience, USA) were subcutaneously implanted into female, six- to eight-week-old immunodeficient (NOD.Cg-Prkdc^{scid} Il2rg^{tm1Wjl}/SzJ) mice³⁵ under IACUC approval (100533-

1115) To test spontaneous transformation of the stem cells, mice were monitored every month (up to 4 months).

RNA and genomic DNA sample preparation. For stem cell colonies, RNA was isolated using PicoPure RNA Isolation Kit (Life Technologies, USA). For ALI-differentiated epithelia, RNA was isolated using TRIzol RNA Isolation Kit (Life Technologies, USA). RNA quality (RNA integrity number, RIN) was measured by analysis Agilent 2100 Bioanalyzer and Agilent RNA 6000 Nano Kit (Agilent Technologies, USA). RNAs having a RIN > 8 were used for microarray analysis. Genomic DNA was extracted with DNeasy Blood & Tissue kit (Qiagen, Netherlands) from intestinal and colonic stem cells for CNV analysis and exome capture sequencing. For genomic DNA extraction, human intestinal and colonic stem cells were isolated from mouse 3T3 feeder layer using QuadroMACS Starting Kit (Miltenyi Biotec, Germany). Genomic DNA concentration was measured with Qubit dsDNA BR Assay Kit (Life Technologies, USA).

Expression microarray and bioinformatics. Total RNAs obtained from immature colonies and ALI-differentiated structure were used for microarray preparation with WT Pico RNA Amplification System V2 for amplification of DNA and Encore Biotin Module for fragmentation and biotin labelling (NUGEN Technologies, USA). RNA quality (RNA integrity number, RIN) was measured by analysis using an Agilent 2100 Bioanalyzer and Agilent RNA 6000 Nano Kit (Agilent Technologies, USA). RNAs having a RIN > 8 were used for microarray analysis. All samples were prepared according to manufacturer's instructions and hybridized onto GeneChip Human Exon 1.0 ST Array (Affymetrix, USA). GeneChip operating software was used to process all the Cel files and calculate probe intensity values. To validate sample quality, quality checks were conducted using Affymetrix Expression Console software. The intensity values were log₂-transformed and imported into the Partek Genomics Suite 6.6 (Partek Incorporated, USA). Exons were summarized to genes and a 1-way ANOVA was performed to identify differentially expressed genes. For two-sample statistics, *P* values were calculated by Student's *t*-test for each analysis. Unsupervised clustering and heat map generation were performed with sorted data sets by Euclidean distance based on average linkage clustering, and principal component analysis (PCA) map was conducted using all or selected probe sets by Partek Genomics Suite 6.6. Gene set enrichment analysis (GSEA)⁵³ was performed for *C. difficile* toxin B treatment. For the region-specific gene signature of small intestine and colon comparison (PD, PJ and MI for Fig. 2b and AC, TC and DC for Fig. 3b), differentially-expressed genes were selected with a cut-off value of 1.5-fold and *P* < 0.05 in each comparison (for example, (1) PD vs. PJ and (2) PD vs. MI) and then intersected genes in 2 gene lists of each comparison were taken as region-specific gene sets. In the heat maps (Fig. 2b and 3b), 3 regionspecific gene sets (PD, PJ and MI, or AC, TC and DC) were combined, and the heat maps were made with Euclidean distance based on average linkage clustering. For *C. difficile* toxin B treatment data sets, samples from indicated time points and dosages were compared with control (untreated samples). Differentially-expressed genes (two-fold upregulated and downregulated genes) were counted and plotted in 3D column plots (Extended Data Fig. 8c). In comparison of 500 pM 24 h toxin B treatment with control, 39 genes were significantly upregulated (cut-off value: 3-fold and *P* < 0.05) and a heat map (Fig. 6e) was made with 39 genes using all samples. The whole genome expression data of 500 pM 24 h toxin B treatment vs. control were applied to GSEA program to detect significantly enriched pathway in toxin B treatment. Selected pathways (from KEGG) were shown in Fig. 6d. Data sets generated for this study have been submitted to the National Center for Biotechnology Information Gene Expression Omnibus (GEO) database under accession number GSE66749.

No statistical methods were used to predetermine sample size.

Copy number variation. For copy number variation analysis of stem cell pedigrees and passage 0 pooled sample, genomic DNA samples were genotyped with HumanOmniExpress BeadChip Kit for clone 1 and 2 (passage 5, 10, 15 and 20) (Illumina, USA) and Illumina HumanOmniZhonghua BeadChip Kit for clones 3 to 7 (passage 5 and 25) following the manufacturer's instructions. Analysis of BeadChip was performed using GenomeStudio Software (Illumina, USA). Illumina high-density SNP genotyping data was converted to kilobase-resolution detection of copy number variation. CNV detected in passage 0 pooled samples are considered as germline CNVs and removed in the analysis. The data was generated by PennCNV⁵⁴. Genes within 10 kb of CNV regions are reported. The parameter is set as “-expandleft 10k” and “-expandright 10k”. Other parameters are default. Confidence score >10 was used as a cutoff. The call rates for CNV were all greater than 99%, and two larger CNV amplification and deletion events were validated by quantitative PCR.

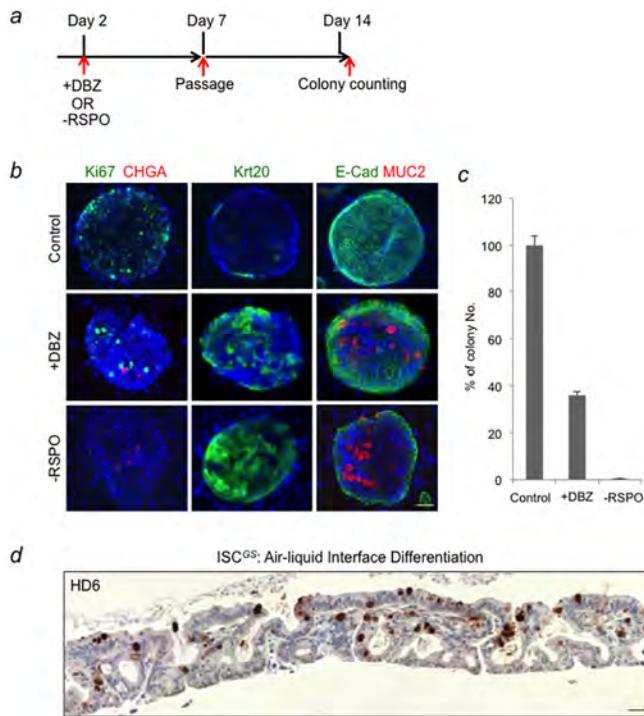
Exome capture sequencing. For exome capture and high-throughput sequencing for intestinal stem cells (pedigree 1 and 2), 50 ng of genomic DNA was used to perform Nextera Expanded Exome Kit (Illumina, USA). For pedigree 3 to 7, 1 μg of genomic DNA was sheared using a Covaris S1 Ultrasonicator (Covaris, USA),

end-repaired, A-tailed, and Adaptor-ligated. Exome capture was performed using a Tru-seq Exome Enrichment Kit (Illumina, USA) following the manufacturer's instructions. Multiplexed libraries were sequenced on an Illumina HiSeq sequencer using 101-bp paired-end reads. Reads were aligned to the reference genome (UCSC hg19) using Burrows Wheeler Aligner (BWA, 0.6.2)⁵⁵. PCR duplicates were removed using PICARD-1.94 (<http://picard.sourceforge.net>). The Genome Analysis Toolkit (GATK framework version 2.6.4)⁵⁶ was used to realign reads near indels and to recalibrate base quality values.

When running GATK, the minimum phred-scaled confidence threshold at which variants were called (-stand_call_conf) was 50, and the minimum phred-scaled confidence threshold at which variants were emitted (-stand_emit_conf) is 30. The criteria of GATK Variant Filtration is as follows: --clusterWindowSize 10--filterExpression "MQ0 > 4 && ((MQ0/(1.0*DP)) > 0.1)"--filterName "HARD_TO_VALIDATE"--filterExpression "DP < 5"--filterName "LowCoverage"--filterExpression "QUAL < 30"--filterName "VeryLowQual"--filterExpression "QUAL > 30 && QUAL < 50"--filterName "LowQual"--filterExpression "QD < 1.5"--filterName "LowQD"--filterExpression "FS > 150"--filterName "StrandBias". Potential mouse genomic DNA contaminant reads were detected by alignment to the mouse genome (UCSC mm10) and those containing less than 3 mismatches were removed from further analysis. SNVs were called in each sample separately using SAMtools v0.1.19⁵⁷ and GATK in the exome capture targeted regions. Variants with at least Q50 confidence, phred-scaled quality score more than 40 and coverage higher than 10 were considered as true SNVs. Variants were annotated with ANNOVAR (version 11 Feb, 2013)⁵⁸. Identical variant calls in intestinal stem cells (passage 5 and higher) when compared to passage 0 pooled samples were used to identify germline SNVs. Sanger sequencing validation was performed using primers designed with Primer3 software

version 4.0 (<http://frodo.wi.mit.edu/>). Extracted genomic DNA was amplified with titanium Taq polymerase (Clontech Laboratories, CA, USA) and purified PCR products were sequenced in the forward directions using ABI PRISM BigDye Terminator Cycle Sequencing Ready Reaction kits and an ABI PRISM 3730 Genetic Analyzer (Applied Biosystems, CA, USA). We validated by PCR and Sanger sequencing 13 of 14 non-synonymous mutations called by our sequencing efforts suggesting a false discovery rate of less than 10%. Other quality control parameters are shown in Supplementary Information Table 4.

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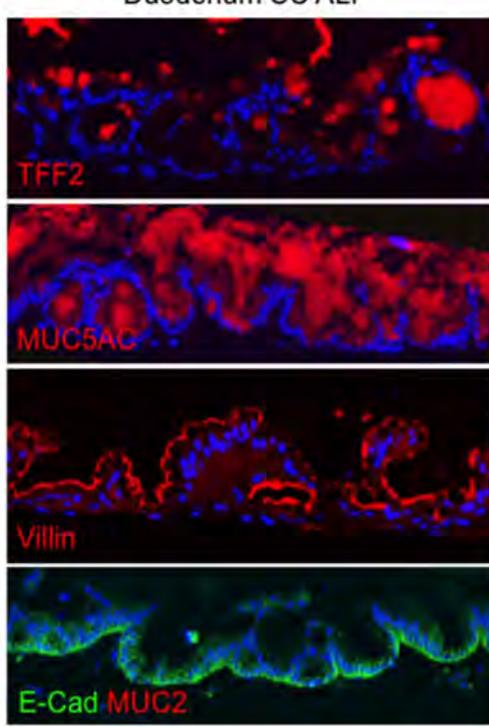
Extended Data Figure 1 | Loss of clonogenicity in differentiated ISC.

a, Schematic of ISC differentiation using either the γ -secretase inhibitor dibenzazepine (DBZ) or withdrawal of the Wnt regulator R-spondin 1 (Rspo1). ISCs were plated on day 0, DBZ added or Rspo1 removed at day 2, and colonies passaged en masse at day 7. At day 14, after 7 days of continuous growth, colonies were counted. **b**, Micrographs show immunofluorescence at day 7 colonies grown without Rspo1 or in the presence of DBZ for 5 days using antibodies to Ki67, chromogranin A (CHGA), keratin 20 (Krt20), E-cadherin (E-cad), and mucin 2 (Muc2). Scale bar, 50 μ m; $n = 4$ technical replicates. **c**, Histogram shows colony formation in each condition normalized to control ISCs. $n = 4$ biological replicates; error bars, s.d. **d**, Staining of ALI-differentiated intestinal stem cells with monoclonal antibody HD6 directed to Paneth cells. Scale bar, 50 μ m; $n = 4$ technical replicates.

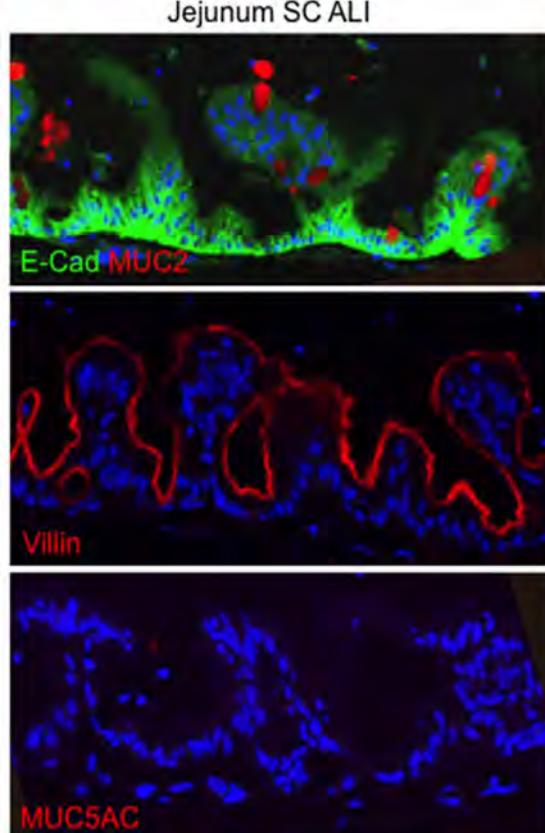
a

Cell types	Gene symbol													
Du-high 133 genes	ABC6	ABHD2	ABHD2	ACOX1	ADAM28	AHNAK	AKR1B10	ALDH3A1	ANXA1	ANXA10	ANXA5	ARHGAP24		
	ARL4C	BACE2	BCAS1	BICC1	BTD	C11orf9	C4orf34	CA2	CAPG	CAPN6	CD24	CD59		
	CLDN18	CNOT7	CRIP1	CTSD	CXCL17	CYP2C18	CYP3A5	CYSTM1	DNM2	DPCR1	EHD2	EPB41L1		
	FAM110B	FAM177B	FAM189A2	FN1	FOSB	FSIP2	FUT9	FXYD3	GALNT3	GALNT7	GNAQ	GPR87		
	GPRC5B	HIPK2	HMGCS2	HOXB8	HS3ST5	HSPB1	HTR1B	IL18R1	IL2RA	KCNE3	KLF4	LEPREL1		
	LGMD	LPAR1	LRP1	LYPD6B	MAOB	MEIS2	METTL7A	MFSD1	MITF	MLPH	MSMB	MUC1		
	MXD1	MYEOV	NDUFB1P1	NEK6	NFAT5	NKX6-3	NTRK2	OASL	P4HA1	PART1	PCDH7	PGC		
	PLA2G10	PLXNA2	PP7080	PPARGC1A	PSCA	PVRIG	PXDC1	QKI	RAB27B	RBMS1	RERG	RETSAT		
	RGNEF	RHBDL2	RHOBTB1	RNF128	RNF183	ROBO1	S100P	SCIN	SFTA2	SGK2	SLC16A3	SLC19A3		
	SLC26A9	SLC41A2	SLC44A4	SLC45A3	SLC4A4	SLC9A1	SLC9A2	SLC9A3	SMPDL3A	SPINK1	STEAP1	SULT1C2		
	SYT9	TFF1	TF2	TFF3	TM4SF1	TPBG	TRAK1	TSHZ2	TSPAN1	TSPAN31	UGDH	VSIG1		
	VSIG2													
Je-high 24 genes	BDKRB2	C2CD4A	CCR1	CHRM3	CPVL	CYP2A13	EPHB1	FAM47B	FMOD	GLDC	HSD17B7P2	IFITM3		
	LGR5	ODAM	OR8J1	PHYHIPL	RTP4	SESN1	SHPK	SLC26A2	STARD13	TPH1	UNC93A	ZRSR2		
Il-high 178 genes	ABC6	ABCC2	ABCG2	ACE2	ACOX2	ADH4	ADH6	AKAP7	ALDOB	ANPEP	ANXA2P2	APOB		
	AREG	BTNL3	C17orf72	C1orf201	C1orf21	C3orf26	C3orf52	C4BPB	CACNA1E	CCL25	CCND2	CD52		
	CDH17	CDX2	CEACAM1	CEACAM5	CELA3A	CELA3B	CHGA	CIDE	CLCA1	CLIC5	CLRN3	CPE		
	CSF1R	CYBRD1	CYP2A7	DACH1	DENND1A	DHRS11	DKK1	DMBT1	DOK3	DPP4	DSG3	DUSP5		
	EFCAB4B	EGR2	EML1	EREG	F2R	FABP2	FABP6	FAM105A	FCGBP	FGF23	FITM2	FOLH1		
	FRZB	GALNT8	GBA3	GCET2	GDAP1	GFOD1	GHRL	GIP	GJA1	GLS	GPA33	GSDMB		
	GSTA2	GUCY2C	HEPACAM2	HHLA2	HLA-DRB1	HNF4G	HTR1D	IL18	IL2RG	IL32	INE1	IRF8		
	ITLN1	JAG1	KIAA0226L	KIRREL	KLF7	KRT20	KRT33B	KRT80	L1TD1	LCT	LEAP2	LGALS2		
	LGALS3	LINC00483	LOC100132099	MANBAL	MAOA	MARCH3	MARCH8	MB21D2	MEP1A	MEP1B	MICAL2	MIR17HG		
	MLN	MOGAT3	MRPS18A	MUC13	MUC17	MYO1A	MYO1E	MYO7B	NABP1	NELL2	NIPAL1	NME5		
	NODAL	NOX1	NPY6R	NR1H4	O3FAR1	OSR2	OSTBETA	OSTalpha	OTC	PAD12	PAPSS2	PDE10A		
	PDE3A	PDP1	PI3	PLA2G12B	PLK1S1	PMP22	PRAP1	RASGRF2	RBP2	RGS2	RHOB	RNF182		
	RNF217	SARM1	SATB2	SEMA3D	SEMA6D	SERTAD1	SI	SIDT1	SLC17A4	SLC2A5	SLC30A2	SLC46A3		
	SLC6A20	SLC7A6	SNX10	TCEANC	TGFB1	THEM4	TM4SF20	TM6SF2	TMEM45B	TRIM36	TUBAL3	TUFT1		
	UGT2B15	VTN	XDH	YAE1D1	ZG16	ZNF208	ZNF347	ZNF502	ZNF705G	ZYX				

b

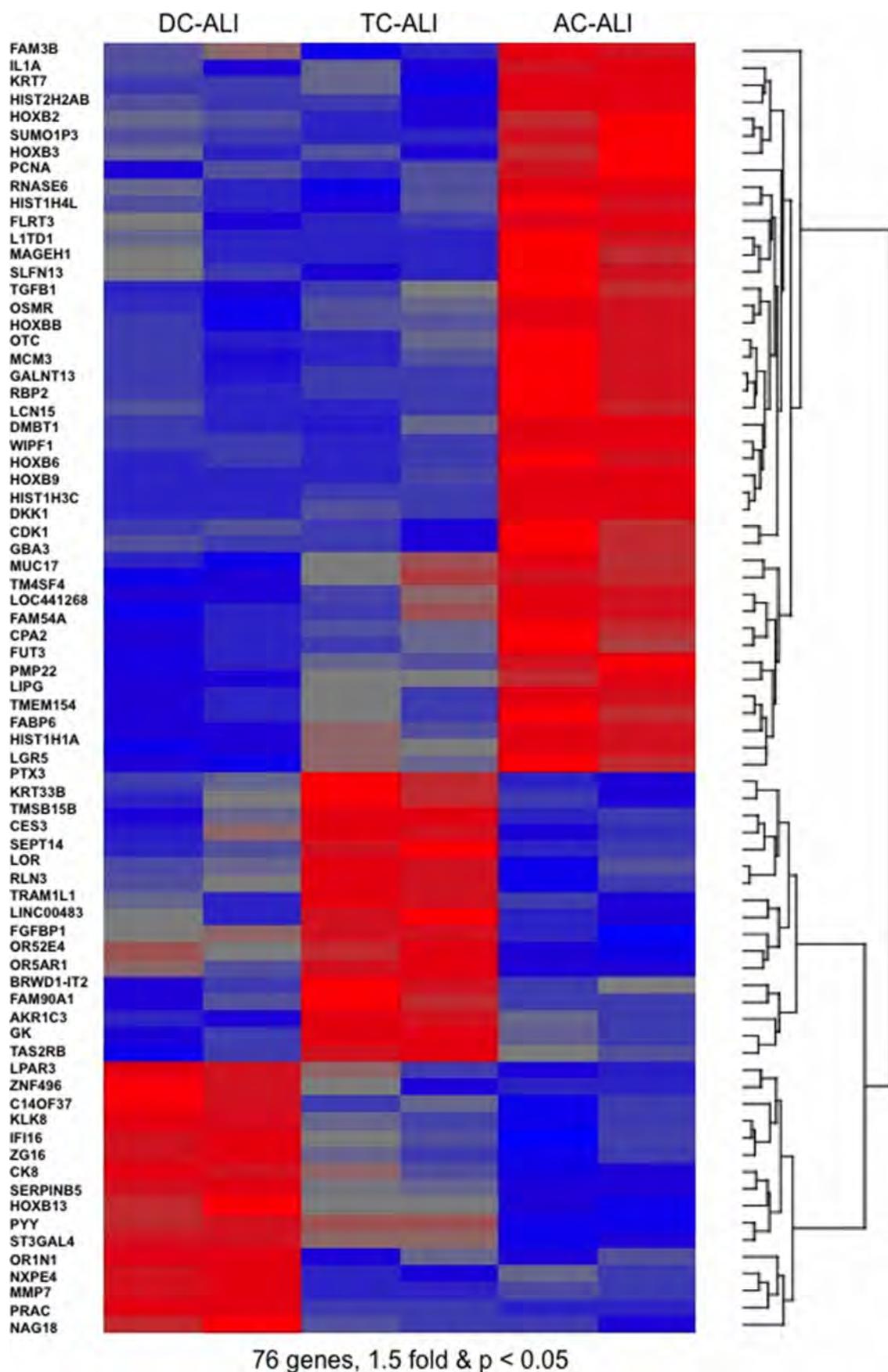


c

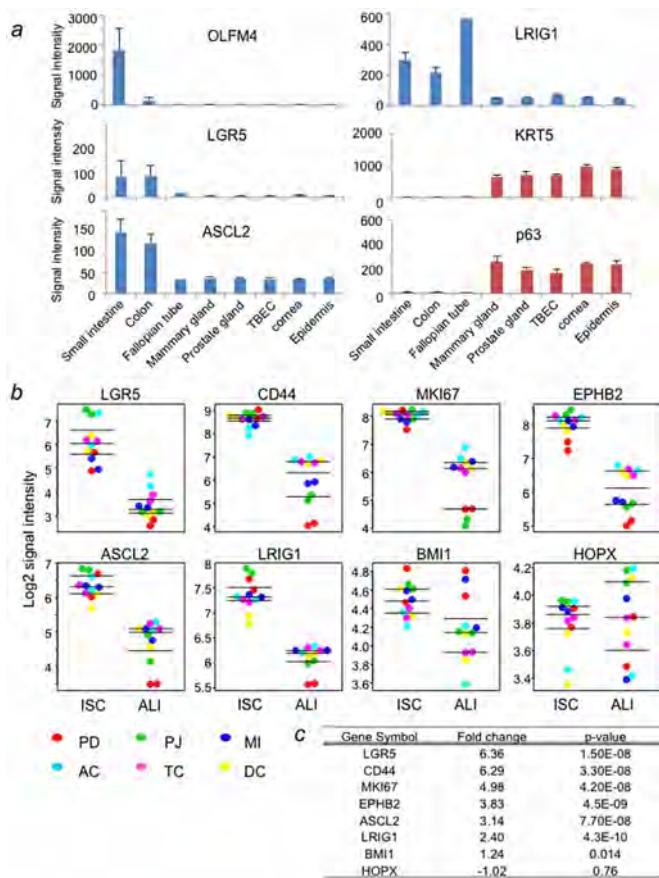


Extended Data Figure 2 | Intestinal stem cell expression profiles. a, List of genes differentially expressed in ISC derived from duodenum, jejunum and ileum. These data correspond to heat map of Fig. 2b. b, Immunofluorescence labelling of ALI-differentiated ISC from duodenum with antibodies against

Tff2, mucin 5AC, villin, E-cadherin, and mucin 2. c, Immunofluorescence labelling of ALI-differentiated epithelia from jejunum stem cells with antibodies to E-cadherin, mucin 2, villin, and mucin 5AC. Scale bar, 50 μ m; $n = 10$ technical replicates.



Extended Data Figure 3 | Differential gene expression in epithelia derived from colonic stem cells. Heat map of differentially expressed (>1.5 -fold, $P < 0.05$) genes in ALI cultures derived from stem cell pedigrees of ascending, transverse, and descending colon.



Extended Data Figure 4 | Differential gene expression across columnar and stratified epithelial stem cells. **a**, Histograms of expression microarray signal intensity of selected genes across averaged intestine and colon ISCs, stratified epithelial stem cells, and stem cells of the fallopian tube (FT). Biological replicas $n = 2-6$ (FT = 2, stratified epithelia = 3, colon, intestine = 6); error bars, s.d. **b**, Dot plot showing expression microarray data of indicated genes for stem cell pedigrees (ISC; Duo, duodenum; Jej, jejunum; Ile, ileum; AC, ascending colon; TC, transverse colon; DC, descending colon) derived from various regions of the intestinal tract before and after air–liquid interface (ALI) differentiation. Biological replicas $n = 2$ (total 12 data sets) for stem cells, technical replicas $n = 2$ for ALI. **c**, Chart of aggregate P values by Student's t -test for gene expression changes between ground state stem cells and their ALI-differentiated counterparts.

a CNVs and SNVs in 2 clones of Fetus-1

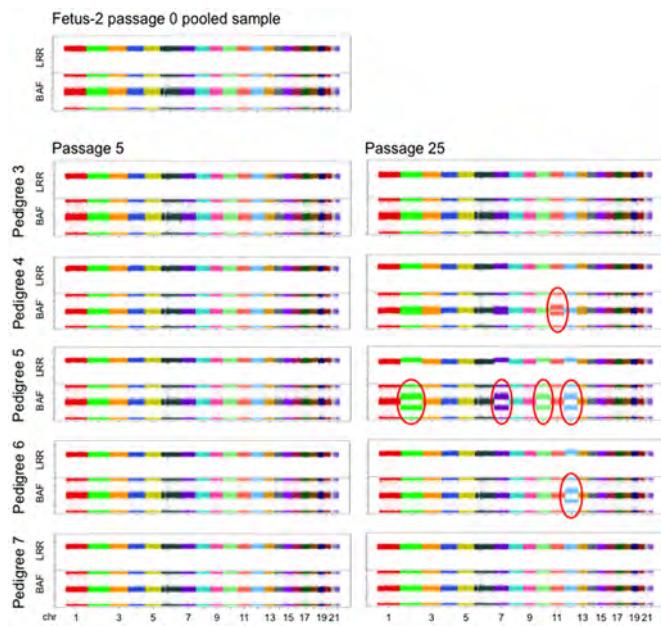
b Gene list for CNVs in 5 clones of Fetus-2

Genes affected by amplification	Gene symbol
Pedigree 3 P5	No genes
P25	Clu1011
Pedigree 4 P5	ACAP2
P25	Chr 11 transcript
Pedigree 5 P5	SEPECS
P25	Chr 2, 7, 10 and 12 transcripts
Pedigree 6 P5	No genes
P25	SATB1
Pedigree 7 P5	No genes
P25	LOC152205

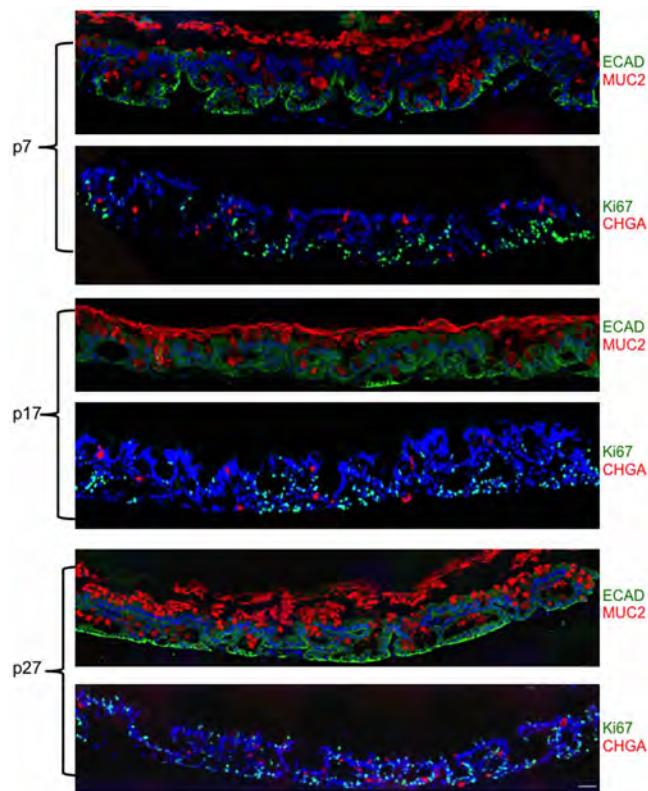
C Gene list for SNVs in 5 clones of Fetus-2

Gene list for C4V9 in 3 clones of Cetus-2	Clone No.	Passage	Gene symbol of homologous mouse
Pedigree 3	Passage 5	BSN	
		Passage 25	KIAA0226 ATP7A
Pedigree 4	Passage 5	RBMXL1	
		Passage 25	DCK10 CXCR7
Pedigree 5	Passage 5	FAM135A	
		Passage 25	CV2P1B2 PTGSS2
Pedigree 6	Passage 5	ASUN	CDH8
		Passage 25	LRRK37A3
Pedigree 7	Passage 5	KCNM1A	KRTAP8-5 PSMC5
		Passage 25	BPIFC1
Pedigree 8	Passage 5	TMEM48	ANKR017
		Passage 25	ANKR017
Pedigree 9	Passage 5	CTC1	ATX4
		Passage 25	PVRIL2
Pedigree 10	Passage 5	ECEL1	KIF19
		Passage 25	KRTAP8-1 EP100

Extended Data Figure 5 | Genes affected by CNV and SNV events in intestinal stem cell pedigrees during passaging. **a**, Summary of CNV (events (genes affected)) and non-synonymous SNV in pedigrees 1 and 2 at P5 to P20. **b**, Summary of genes altered by interstitial CNV amplifications (top) or deletions (bottom) in ISC pedigrees 3 to 7 at P5 and P25. **c**, Summary of genes sustaining non-synonymous SNV in five ISC pedigrees at P5 and P25.



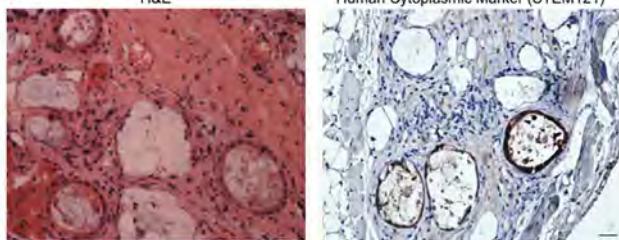
Extended Data Figure 6 | Whole-genome CNV profiles for intestinal stem cell pedigrees 3–7 at P5 and P25. Regions marked by ovals represent aneuploidy.



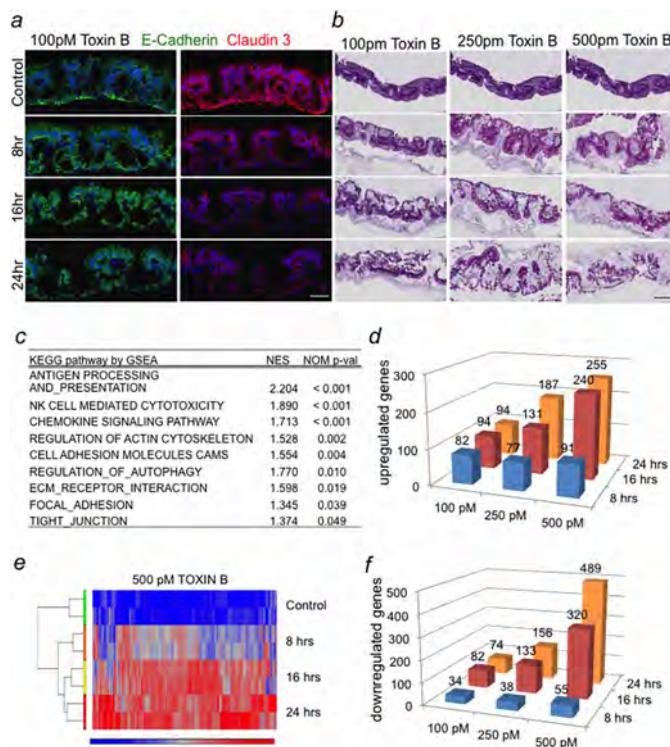
Extended Data Figure 7 | Impact of ISC^{GS} passaging on ALI differentiation.
ALI differentiation of intestinal pedigree 2 initiated from cells at the indicated passage number. As indicated, histological sections of differentiated epithelia were stained with antibodies to either E-cadherin (ECAD, green) and mucin 2 (Muc2, red), or Ki67 (green) and chromogranin A (CHGA, red). Scale bar, 75 μ m; $n = 4$ technical replicates.

a

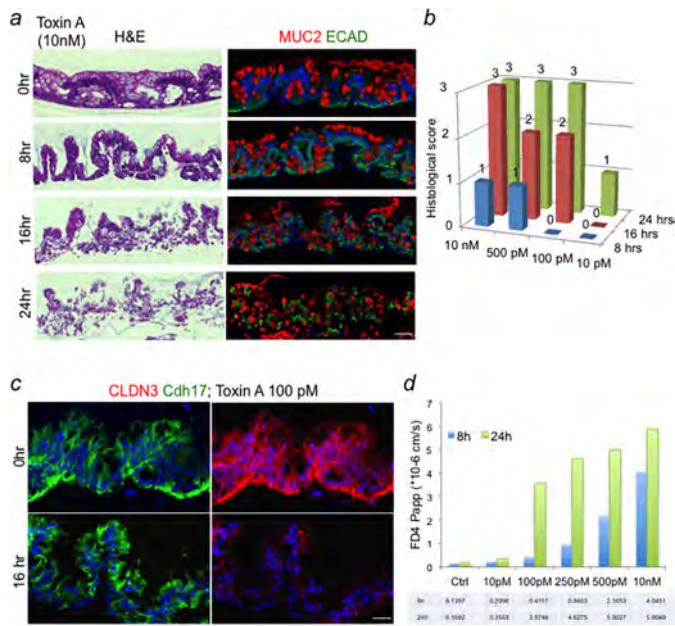
Name	Time wks	4 wks	8 wks	12 wks	16 wks
Pedigree 3 P6		0/2	0/2	0/2	0/2
Pedigree 3 P25		0/2	0/2	0/2	0/2
Pedigree 5 P6		0/2	0/2	0/2	0/2
Pedigree 5 P25		0/2	0/2	0/2	0/2
Pedigree 7 P6		0/2	0/2	0/2	0/2
Pool		0/2	0/2	0/2	0/2
Cancer Cells		0/8	2/8	5/8	8/8

b

Extended Data Figure 8 | ISC^{GS} tumorigenicity assays in immunodeficient mice. **a**, Quantification of tumour formation assessments at 4–16 weeks following subcutaneous inoculation of two million cells of the indicated ISC pedigrees at passage 6 or passage 25 at 4–16 weeks. ‘Pool’ indicates total set of clones derived from P0 ileum culture before pedigree generation. ‘Cancer cells’ refers to propagating cells from case of high-grade serous ovarian cancer. **b**, Left, histological section through site of injection of 1 million cells from pedigree 3. Right, section of injection site stained with antibody (STEM121) to human epithelial cells (brown) revealing benign cysts. Scale bar, 15 μ m.



Extended Data Figure 9 | Dose- and time-dependency of TcdB pathology in ALI-generated colonic epithelia. **a**, Immunofluorescence localization of adherens junction marker E-cadherin and tight junction marker claudin 3 in ALI-differentiated epithelia derived from transverse colon stem cells following exposure to 100 pM TcdB for the indicated durations. $n = 4$ technical replicates. Scale bar, 100 μ m. **b**, Representative H&E images of ALI cultures at indicated times and concentration of TcdB exposure. Scale bar, 250 μ m; $n = 4$ technical replicates. **c**, Gene set enrichment analysis of whole-genome expression data from colonic epithelia treated with 500pM TcdB for 24 h and control samples showing enriched KEGG pathway sets. NES, normalized enrichment score; NOM P value, nominal P value. **d**, 3D plot of upregulated genes at the indicated time points and dosages $>$ twofold, $P < 0.05$. $n = 2$ technical replicates. **e**, Heat map of upregulated genes in 500 pM TcdB samples. The genes (237 genes) were chosen by cutoff values ($>$ twofold, $P < 0.05$). Three time points (8, 16 and 24 h) are shown. **f**, 3D plot of downregulated genes at the indicated time points and dosages $>$ twofold, $P < 0.05$. $n = 2$ technical replicates.



Extended Data Figure 10 | Dose- and time-dependency of TcdA pathology in ALI-generated colonic epithelia. **a**, Left, representative H&E images of ALI cultures at indicated times and concentration of TcdA exposure; right, immunofluorescence localization of adherens junction marker E-cadherin (ECAD; green) and mucin 2 (MUC2; red) in ALI-differentiated epithelia derived from transverse colon stem cells following incubation with 10 nM TcdA for the indicated durations. Scale bar, 100 μ m; $n = 4$ technical replicates. **b**, 3D plot of histological scoring of representative H&E time points and concentrations performed by a gastrointestinal pathologist according to a standard 0–3 rating for colonic epithelial integrity. **c**, Distribution of tight junction marker claudin 3 (Cldn3) and adherens junction marker (Cdh17) following treatment of ALI colonic epithelium with TcdA for the indicated times and doses. Scale bar, 50 μ m; $n = 4$ technical replicates. **d**, Histogram of permeability of ALI colonic epithelium (Papp) to small molecules (FD4, molecular mass 4,400 Da) following exposure to the indicated doses of TcdA for the indicated times.

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Evidence for a Dualistic Model of High-grade Serous Carcinoma

BRCA Mutation Status, Histology, and Tubal Intraepithelial Carcinoma

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James E. Conner, MD, PhD,* Stephanie Schulte, MD, PhD,* Neil Horowitz, MD,‡§

Christopher P. Crum, MD,* and Emily E. Meserve, MD, MPH*

Abstract: Most early adnexal carcinomas detected in asymptomatic women with germline *BRCA* mutations (*BRCA*⁺) present as serous tubal intraepithelial carcinomas (STIC). However, STICs are found in only 40% of symptomatic high-grade serous carcinomas (HGSCs) and less frequently in pseudoendometrioid variants of HGSC. Consecutive cases of untreated HGSC from *BRCA*⁺ and *BRCA*⁻ women with detailed fallopian tube examination (SEE-FIM protocol) were compared. STIC status (+/−) was determined, and tumors were classified morphologically as SET (“SET”, >50% solid, pseudoendometrioid, or transitional) or classic predominate (“Classic”). SET tumors trended toward a higher frequency in *BRCA*⁺ versus *BRCA*⁻ women (50% vs. 28%, $P = 0.11$), had a significantly younger mean age than those with classic HGSC in *BRCA*⁻ women (mean 56.2 vs. 64.8 y, $P = 0.04$), and displayed a better clinical outcome in both groups combined ($P = 0.024$). STIC was significantly more frequent in tumors from the *BRCA*⁻ cohort (66% vs. 31%, $P = 0.017$) and specifically the *BRCA*⁻ tumors with classic morphology (83%) versus those with SET morphology (22%, $P = 0.003$). Overall, several covariates—histology, *BRCA* status, age, coexisting STIC, and response to therapy—define 2 categories of HGSC with differences in precursor (STIC) frequency, morphology, and outcome. We introduce a dualistic HGSC model that could shed light on the differences in frequency of STIC between symptomatic and asymptomatic

women with HGSC. This model emphasizes the need for further study of HGSC precursors to determine their relevance to the prevention of this lethal malignancy.

Key Words: fallopian tube, neoplasia, serous carcinoma, *BRCA*, endometrioid, tubal intraepithelial carcinoma, risk-reduction salpingo-oophorectomy

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In the last decade, the origin of ovarian cancer has become the subject of intense study, and the distal fallopian tube has emerged as a potential origin for a significant proportion of high-grade serous carcinomas (HGSCs).^{1,2} Evidence in support of the distal fallopian tube as a site of origin has been (1) the discovery of tubal epithelial atypia in women with *BRCA1* or *BRCA2* mutations, (2) detection of high-grade serous tubal intraepithelial neoplasia (STIC) in risk-reducing salpingo-oophorectomies (RRSOs), (3) the finding of STIC in fallopian tubes of women with advanced carcinoma, and (4) identification of a credible precursor spectrum spanning both normal and neoplastic tubal mucosa.^{1,3–5} The latter has been characterized by evidence of DNA damage, *p53* mutation, and progressive molecular perturbations that have been reproduced in both cell culture and animal models.^{6–8}

The percentage of HGSCs whose origins can be traced to the distal fallopian tube has increased, in part attributable to the use of sampling protocols (SEE-FIM) that more thoroughly examine the distal fallopian tube and fimbria. Identification of STIC supports, if not confirms, a tubal origin in 18% to 60% of cases of advanced or symptomatic HGSCs.² Still, in a significant percentage of cases, a tubal carcinogenic sequence has not been confirmed by detection of an intramucosal carcinoma. In contrast, when HGSCs are discovered early or in asymptomatic women (RRSO), approximately 80% coexist with STIC.^{9–11}

In recent publications, the spectrum of HGSC has been expanded to include endometrioid or endometrioid-like (pseudoendometrioid) tumors, largely because of the observation of an identical immunophenotype using *p53*, *PTEN*, and *Pax2* as well as similar rates of *p53* mutation.¹² Of interest, Roh et al¹³ found that the

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C.P.C. and E.E.M. contributed equally.

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1 endometrioid subset had a lower frequency of associated
 3 STIC. This finding was of borderline statistical sig-
 5 nificance but raised the possibility that certain tumor
 7 morphologies might be less likely to arise from STIC.
 9 Recently, Soslow et al¹⁴ reported that particular patterns
 11 of HGSC ~~differentiation~~, namely solid, pseudoendome-
 13 trioid, and transitional (SET; Fig. 1), were seen more
 15 commonly in association with *BRCA1/2* mutations. This,
 17 combined with the observations of Roh and colleagues,
 suggested that endometrioid or SET histology might not
 only be more commonly found in women with *BRCA*⁺
 mutations but paradoxically less likely to be associated
 with a STIC as currently described. The purpose of this
 study was to examine this paradox from the perspective of
 symptomatic malignancies in women with (*BRCA*⁺) and
 without (*BRCA*⁻) germline mutations in the *BRCA1* or
BRCA2 genes.

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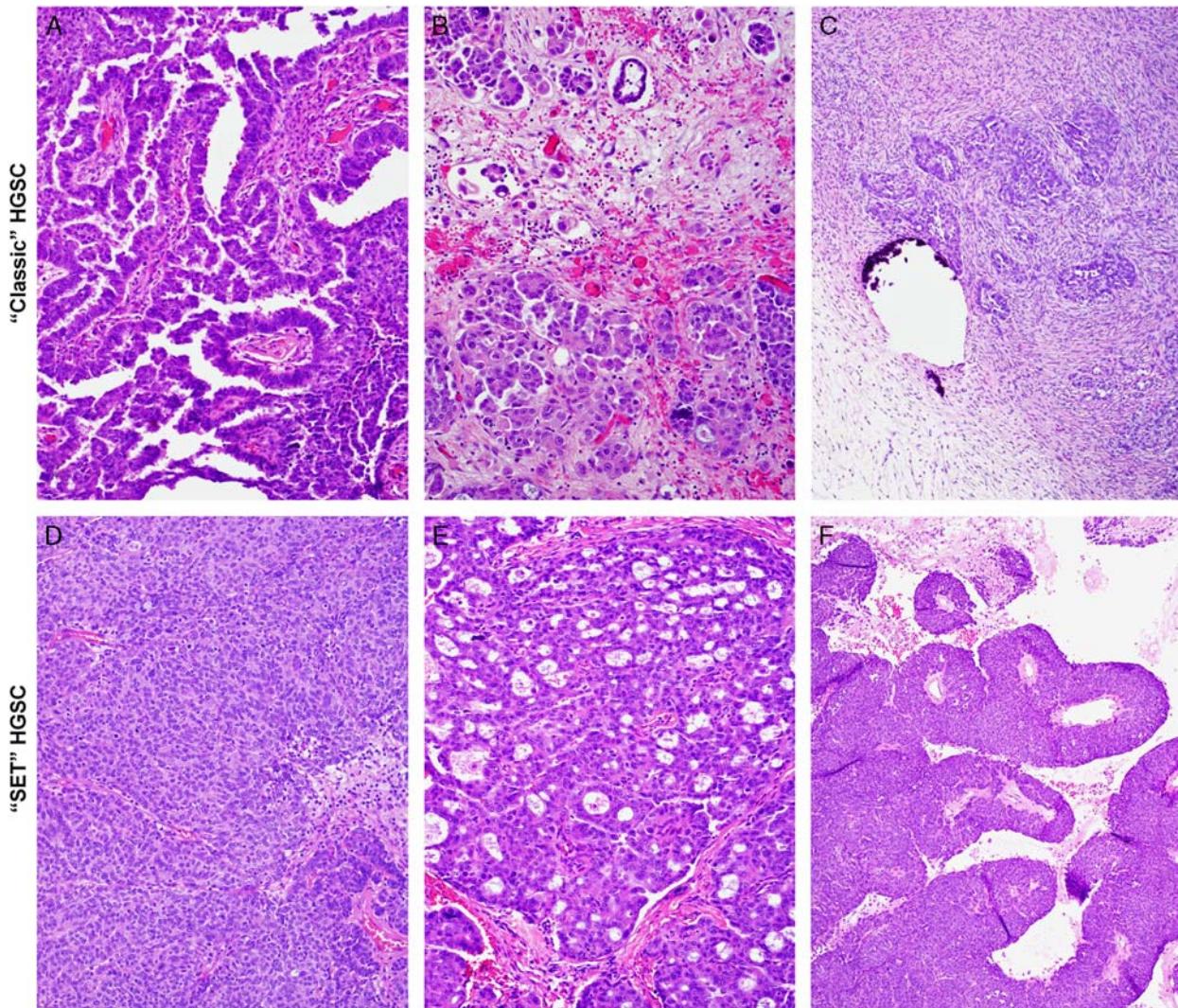
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59 **FIGURE 1.** Histologic features of HGSC. Classic patterns include papillary (A), micropapillary (B), and infiltrative (C). SET patterns
 59 include solid (D), endometrioid-like (E), and transitional (F).

MATERIALS AND METHODS

Patient Samples and Case Selection

This study was approved by the institutional review boards at Brigham and Women's Hospital (BWH) and Dana Farber Cancer Institute (DFCI). All cases of HGSC resected at BWH from 2005 to 2013 were identified from archival records. Careful examination of the tubes and ovaries, including the SEE-FIM protocol, was performed in all cases as previously described.³ This cohort was cross-indexed with genetic testing records in the Center for Cancer Genetics and Prevention at DFCI to identify 2 cohorts of women with HGSC: those who were confirmed to have *BRCA1/2* germline mutations and those documented to be negative for these mutations. Patients who received neoadjuvant chemotherapy were excluded from this study. Between 2005 and 2013, 387

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1 patients underwent surgery at BWH for a diagnosis of HGSC. Within this group, 116 underwent germline testing for *BRCA1* or *BRCA2* mutations. A germline mutation in either *BRCA1* or *BRCA2* (*BRCA*⁺) was detected by direct sequence analysis in 47 patients. No *BRCA1* or *BRCA2* germline mutation was detected in 69 patients (*BRCA*⁻). Forty-one patients had undergone neoadjuvant chemotherapy treatment (10 *BRCA*⁺, 31 *BRCA*⁻) and were excluded from the study. Slides were unavailable for histologic review in 17 cases (11 *BRCA*⁺, 6 *BRCA*⁻). Clinical outcome data including the time to last follow-up, and clinical status at last follow-up were extracted from the electronic medical record.

Histologic Review and Classification

Invasive Tumors

Tumors were reviewed without knowledge of their *BRCA* mutation status and classified as previously described into the following groups by 2 coauthors (B.E.H., C.P.C.):

- *Classic Predominate HGSC Histology ("Classic")*: >50% of the tumor demonstrates papillary, micro-papillary, or infiltrative architecture, and often desmoplastic stroma.
- *SET Predominate HGSC Histology ("SET")*: >50% of the tumor displays 1 or more variant features, including solid growth, gland formation, and papillary transitional patterns.

The percentage of tumor containing SET versus classic histology was estimated in each case (in increments of 10%).

STIC Diagnosis

STIC was identified and confirmed as previously described.^{4,5}

Statistical Analysis

Age and predominant morphologic pattern were compared between *BRCA*⁺ and *BRCA*⁻ women by the Student *t* test and χ^2 test. Age was compared between tumors with SET and classic predominant morphology by the Student *t* test. Subgroup analyses of frequency of STIC were performed by the Fisher exact test. Analysis of survival using Kaplan-Meier curves and log rank tests was performed.

RESULTS

Study Population

The study group comprised 26 *BRCA*⁺ cases including 21 advanced (stage 3-4) and 5 early (stage 1-2) carcinomas and 32 advanced *BRCA*⁻ cases, all of which were evaluated by the SEE-FIM protocol. The 5 early carcinomas were all identified in RRSO specimens. Table 1 summarizes the 2 groups.

In 16 (8 *BRCA*⁺ and 8 *BRCA*⁻) of the 58 cases, a grossly normal-appearing portion of distal fallopian tube was sampled (one half of 1 fimbriated end) for research immediately after excision and before processing. In 6, a

TABLE 1. Summary of *BRCA*⁺ and *BRCA*⁻ Tumor Histology, STIC Status, and Age

	Age (y)	No. STIC ⁺ Cases (%)
<i>BRCA</i> ⁺ (all; n = 26)	52.9*	8 (31)
SET (n = 13)	49.7	3 (23)
Classic (n = 13)	55.4	5 (38)
<i>BRCA</i> ⁻ (all; n = 32)	62.5*	21 (66)
SET (n = 9)	56.2**	2 (22)***
Classic (n = 23)	64.8**	19 (83)***

**P* = 0.0007.

***P* = 0.04.

****P* = 0.003.

STIC was ultimately identified in permanent sections from the main specimen. Ten samples taken for special studies were from specimens in which no STIC was identified in the permanent sections. Of these, 8 were examined by frozen section of the banked tissue, none of which revealed a STIC. No pathologic information was available on the remaining 2 samples taken for special studies.

BRCA⁺ Women With HGSC Are Significantly Younger Than *BRCA*⁻ Women

The study group included 17 women with *BRCA*¹ and 9 with *BRCA*² mutations. The mean age of *BRCA*⁺ women was 52.9 years (range 42 to 76 y) and was significantly younger than that of the *BRCA*⁻ population (62.5 y; range 38 to 80 y, *P* = 0.0007).

BRCA⁺ Tumors Trend Toward a Higher Frequency of SET Morphology

Figure 2 and Table 1 summarize the comparison of *BRCA*⁺ and *BRCA*⁻ patients by predominant morphologic pattern. *BRCA*⁺ tumors were more likely to have SET morphology (50%) when compared with *BRCA*⁻ tumors, of which 28% were SET predominate (*P* = 0.11).

In *BRCA*⁻ Tumors, SET Morphology Is Seen in Younger Patients Compared With Those With Classic Morphology

Within the *BRCA*⁻ cohort, tumors with SET morphology had a younger mean age compared with those with classic morphology (56.2 vs. 64.8 y, *P* = 0.04). The *BRCA*⁺ patients with SET morphology tended to be younger (mean 49.7 vs. 55.4 y), although this difference was not statistically significant (*P* = 0.13).

SET Morphology in *BRCA*⁻ Tumors Is Less Likely to be Associated With STIC

Figure 2 and Table 1 summarize and graphically illustrate the frequency and morphology of STIC in *BRCA*⁺ and *BRCA*⁻ tumors. Eight of 26 (31%) *BRCA*⁺ and 21 of 32 (66%) *BRCA*⁻ tumors contained STIC (*P* = 0.017). In the *BRCA*⁺ group, 38% and 23% of classic and SET tumors, respectively, were associated with STIC (*P* = 0.3). In contrast, 83% and 22% of classic and SET *BRCA*⁻ tumors were associated with STIC, respectively (*P* = 0.003). When both *BRCA*⁺ and *BRCA*⁻ groups were combined, the frequency of STIC in

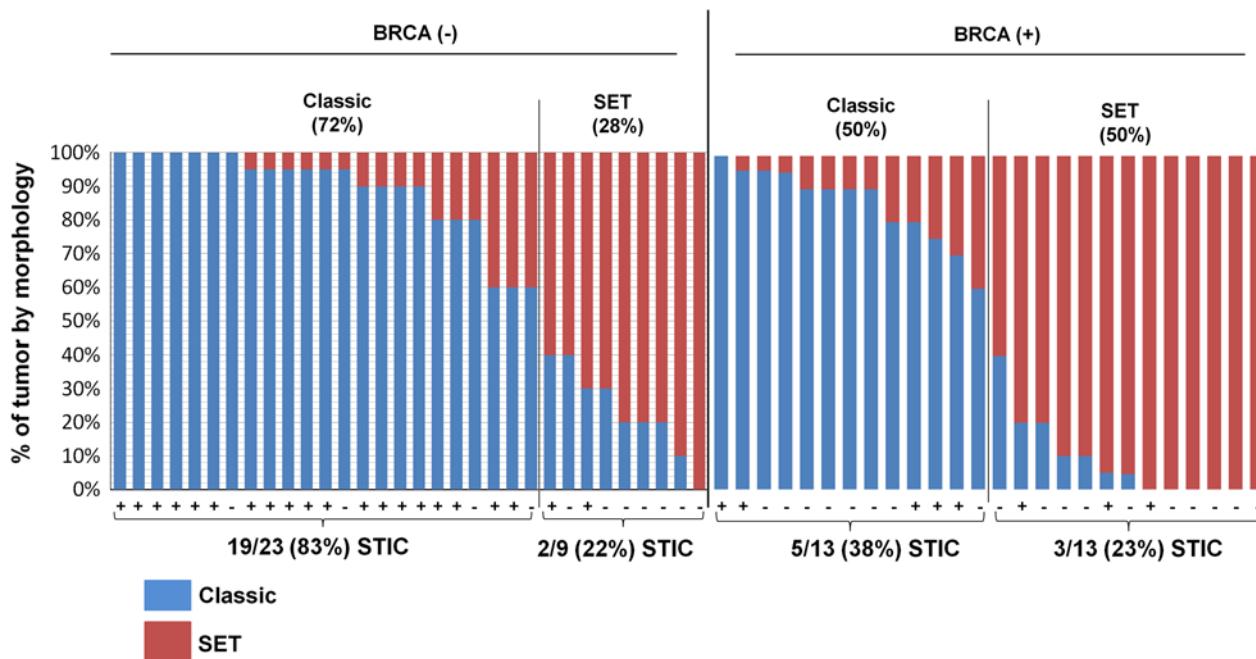


FIGURE 2. Comparison of BRCA^+ and BRCA^- patients by predominant ($> 50\%$) morphologic pattern and STIC status. Each column represents a single patient's tumor, with percent tumor demonstrating SET morphology quantified in red and classic morphology in blue.

classic and SET tumors was 67% and 23%, respectively ($P = 0.003$).

Although most STICs associated with SET tumors were morphologically indistinguishable from those with classic tumors, 1 BRCA^+ case revealed a STIC with a more solid morphology similar to that seen in the associated SET tumor (Fig. 3). The significance of this is unclear at this point.

Clinical Outcome of Tumors With SET Versus Classic Morphology

Table 2 summarizes the clinical outcome of advanced cases with SET versus classic morphology. In general, BRCA^+ patients were less likely to be dead of disease (DOD) at last clinical follow-up; however, 1 BRCA^+ patient with SET morphology who died also had widely metastatic breast carcinoma and so was excluded from this analysis. Five BRCA^+ HGSCs were early stage and detected in RRSO and were also excluded from the clinical outcome analysis. Of note, 4 of 5 (80%) early HGSCs demonstrated SET predominant morphology, whereas 1 of 5 (20%) demonstrated a predominantly classic pattern. All 5 of these BRCA^+ patients were alive without evidence of disease (ANED) at last follow-up (mean 72.5 mo; range 48.3 to 106.5 mo). Of the BRCA^+ patients with advanced disease (mean follow-up time 48.5 mo; range 6.4 to 107.2 mo), 5 of 9 (56%) patients with SET tumors were ANED, in contrast to 3 of 12 (25%) patients with classic morphology who were ANED. Within the BRCA^- cohort (mean follow-up time 30.4 mo; range 8.5 to 55.5 mo), a favorable effect on clinical outcome was seen in patients with SET predominant tumors when compared with those

with classic morphology (1/12 [8%] DOD vs. 8/20 [40%] DOD). After combining both BRCA^+ and BRCA^- women, SET tumors were significantly more likely to trend toward a less severe outcome ($P = 0.024$, χ^2 test for trend).

DISCUSSION

Beginning in 2000, a wealth of information has progressively linked the distal fallopian tube to the origin of HGSC by the discovery of HGSC precursors in the tubal mucosa. This has produced a paradigm shift in the field of ovarian cancer and prompted recent claims that this disease can be partially prevented by opportunistic salpingectomy. The strongest endorsement of a tubal origin has been studies of early carcinomas, which are discovered in approximately 5% to 10% of asymptomatic BRCA^+ women; 80% are associated with a tubal intra-epithelial carcinoma (STIC). The distribution of disease in this early "snapshot" of HGSC was heavily weighted toward the fimbria and prompted speculation that the tube was responsible for virtually all HGSCs. However, 2 subsequent observations suggested that the pathogenesis (and possibly origin) of HGSC is more complex. First, a multitude of studies on average have detected STICs in only 40% (on average) of advanced HGSC. Second, a study showed that "endometrioid" variants of HGSC had a lower frequency of STIC (8%) than HGSC with classic morphology, albeit not significant ($P = 0.09$).¹³ Another study showed that tumors with SET morphology (solid, pseudoendometrioid, transitional) were more likely to be associated with BRCA^+ status.¹⁴ Taken together, these studies raised the possibilities that the pathway to HGSC

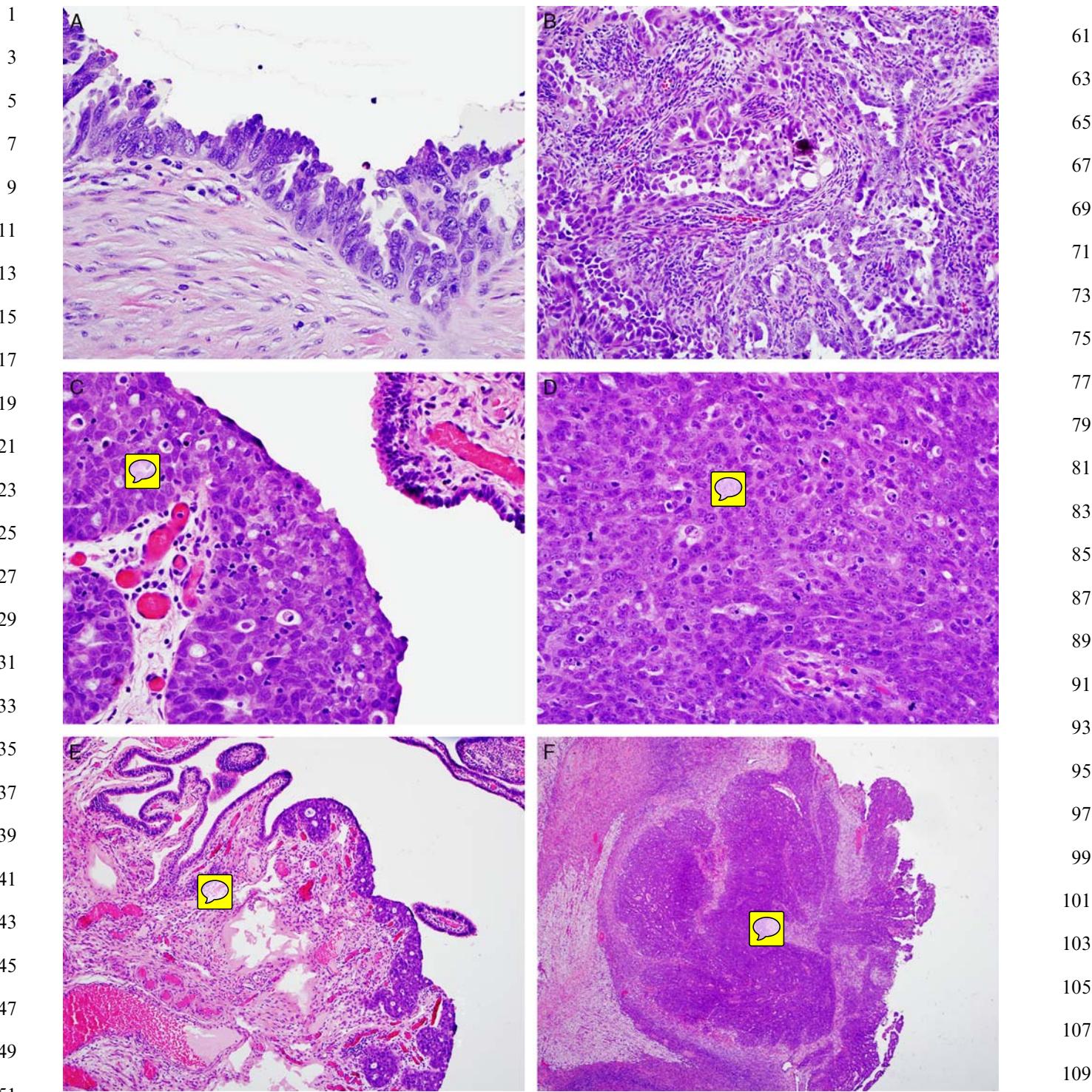


FIGURE 3. Histology of intraepithelial carcinoma (A, C, E) and associated invasive tumor (B, D, F) in a *BRCA*⁻ (A and B) case and *BRCA*⁺ (C-F) case. At higher magnification, the similarity in morphology of 1 *BRCA*⁺ STIC (E) and associated tumor with SET morphology (F) is evident.

55 might be more diverse than expected, both in precursor
56 and cell type.

57 This study establishes further that HGSC, in both
58 *BRCA*⁺ and *BRCA*⁻ women, is not a homogenous disease.

59 In our study of *BRCA*⁺ and *BRCA*⁻ groups, we found that
60 several variables, including histology, coexisting STIC, age,
61 and clinical outcome segregated 2 general tumor groups.
62 Further studies will be needed to flesh out the particulars,

1 **TABLE 2.** Clinical Outcome in Advanced HGSC by *BRCA*
2 Status and Tumor Morphology

	<i>BRCA</i> ⁺		<i>BRCA</i> ⁻	
	SET	Classic	SET	Classic
ANED	5	3	6	4
AWD	1	7	5	8
DOD	2	2	1	8
Total	9	12	12	20

11 SET tumors displayed a statistically significant trend toward a more favorable
outcome ($P = 0.024$, χ^2 test for trend).

12 AWD indicates alive with evidence of disease.

15 but the following observations from this study—witnessed in
17 both *BRCA*⁺ and/or *BRCA*⁻ tumors—suggest >1 form
19 of HGSC: (1) Multiple histologic patterns are observed in
21 HGSC, and the SET pattern seems more common in
23 *BRCA*⁺ women albeit the significance of this association
25 varies depending on the criteria for defining SET morphology
27 and the study population.¹⁴ (2) A significant inverse correlation
29 exists between SET histology and STIC in *BRCA*⁻ tumors. (3) SET histology in *BRCA*⁻ tumors is
associated with a significantly younger mean age. (4) A
generally more favorable outcome exists for women with
SET histology. Further study is warranted to determine
whether there is a consistent association of SET histology
with chemo-responsiveness and whether the SET group of
HGSCs explains why *BRCA*⁺ tumors are generally more
chemo-responsive.

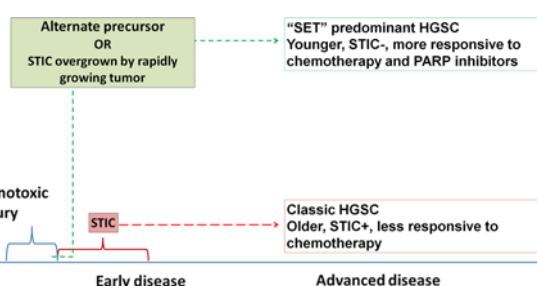
31 The negative correlation between SET histology and
33 coexisting STIC observed in both *BRCA*⁺ and *BRCA*⁻
35 tumors in this study suggests that the differences in
37 morphology may reflect different pathways of tumor evolution.^{13,14} First, we found that SET tumors were associated
with a significantly younger mean age than classic HGSCs.
Second, a recent report looking at fallopian tubes from low-

61 risk women who underwent surgery for benign conditions
63 suggests that isolated STICs in asymptomatic women are
more common than previously appreciated.¹⁵ Moreover, in
65 *BRCA*⁺ women STICs in isolation confer a low risk for
67 HGSC, and when HGSC does develop, there is a lag period
69 of 2 to 5 years after discovery of the STIC.^{9,10} The implications
71 are that progression from STIC to HGSC does not always occur, and when it does it may take years. The
73 classic tumors—which have high association with STIC—fit
75 nicely into the model proposed by Brown and Palmer¹⁶ that
77 allows an interval of a few years between initiation of carcinogenesis
79 and symptomatic disease, during which a defined
81 precursor (STIC) develops and evolves. With the observed
83 younger mean age of discovery and lower frequency of
85 STIC, SET tumors do not fit as cleanly into this model.

87 Figure 4 accounts for the possibility of a second
89 pathway to HGSC and depicts a dualistic model of tumor
91 development in HGSC that incorporates the 2 variables of
93 a defined precursor (STIC) and tumor histology (SET vs.
95 classic). At one pole of this model is classic STIC, which
97 develops and may spread, but demonstrates lag phases both
99 from precursor to STIC and from STIC to symptomatic
101 metastatic tumor, leading to an older average age of clinical
103 presentation. At the other pole are SET tumors that could
105 arise from STIC, from some other tubal precursor, or from
107 elsewhere and become clinically apparent at a younger
109 mean age. This admixture of 2 different tumor biologies
111 would explain a prior observation, which is the rather
113 narrow age gap between *BRCA*⁺ women with STIC versus
115 women with more advanced disease.^{9,10}

117 This study separated classic and SET tumors on the
basis of the assignment of the predominant histologic pattern,
and it remains to be determined how this translates
biologically and whether the associations seen will be re-
produced and consistently reveal 2 separable entities.
However, it should be emphasized that type II “ovarian”
cancers (HGSCs) are increasingly being subdivided, and the
notion that these tumors invariably evolve rapidly may be
an oversimplification. For example, in the breast, multiple
pathogenetic tumor types have emerged, with *BRCA1*
disease most frequently associated with a basal (including
triple negative) breast cancer phenotype and an obscure or
particularly high-grade precursor that evolves rapidly.^{17,18}
Another tumor phenotype, luminal A, is associated with
defined precursors, develops more slowly, and as expected
is more likely to be detected on screening studies.¹⁹⁻²¹
Additional studies are introducing dualistic classifications
of HGSC in *BRCA*⁺ and *BRCA*⁻ women that correlate
molecular profiles with outcome.^{22,23} In parallel with ar-
guments for multiple tumor origins, others have divided
tumors prognostically into ovarian surface or tubal origin
on the basis of expression signatures.^{24,25} Such studies beg
the correlation of molecular pathways, tumor morphology,
and outcome with closer examination of the fallopian tube
and its environs to identify novel precursors to explain
different biological behaviors within the spectrum of
HGSC. The answers bear not only on our understanding of
type II HGSCs but also on expectations both from sero-
logic screening and prophylactic salpingectomy.

51 **FIGURE 4.** A summative model of HGSC pathogenesis with
53 respect to clinical features (age, outcome), precursor lesion,
55 and tumor evolution. In this model, tumor morphology in
57 HGSC could signal a greater likelihood of a certain tumor cell
59 origin and/or biological behavior. The classic pathway involves
a STIC and possibly a protracted period from precursor to
HGSC. The SET pathway evolves differently as implied by
lower frequency of STIC and a younger mean age at discovery.
The 2 pathways also seem to differ in terms of responsiveness
to chemotherapy and PARP inhibitors.



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The PAX2-null immunophenotype defines multiple lineages with common expression signatures in benign and neoplastic oviductal epithelium

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Abstract

The oviducts contain high-grade serous cancer (HGSC) precursors (serous tubal intraepithelial neoplasia or STINs), which are γ -H2AX^p- and TP53 mutation-positive. Although they express wild-type p53, secretory cell outgrowths (SCOUTs) are associated with older age and serous cancer; moreover, both STINs and SCOUTs share a loss of PAX2 expression (PAX2ⁿ). We evaluated PAX2 expression in proliferating adult and embryonic oviductal cells, normal mucosa, SCOUTs, Walthard cell nests (WCNs), STINs, and HGSCs, and the expression of genes chosen empirically or from SCOUT expression arrays. Clones generated *in vitro* from embryonic gynaecological tract and adult Fallopian tube were Krt7^p/PAX2ⁿ/EZH2^p and underwent ciliated (PAX2ⁿ/EZH2ⁿ/FOXJ1^p) and basal (Krt7ⁿ/EZH2ⁿ/Krt5^p) differentiation. Similarly, non-ciliated cells in normal mucosa were PAX2^p but became PAX2ⁿ in multi-layered epithelium undergoing ciliated or basal (WCN) cell differentiation. PAX2ⁿ SCOUTs fell into two groups: type 1 were secretory or secretory/ciliated with a 'tubal' phenotype and were ALDH1ⁿ and β -catenin^{mem} (membranous only). Type 2 displayed a columnar to pseudostratified (endometrioid) phenotype, with an EZH2^p, ALDH1^p, β -catenin^{nc} (nuclear and cytoplasmic), stathmin^p, LEF1^p, RCN1^p, and RUNX2^p expression signature. STINs and HGSCs shared the type 1 immunophenotype of PAX2ⁿ, ALDH1ⁿ, β -catenin^{mem}, but highly expressed EZH2^p, LEF1^p, RCN1^p, and stathmin^p. This study, for the first time, links PAX2ⁿ with proliferating fetal and adult oviductal cells undergoing basal and ciliated differentiation and shows that this expression state is maintained in SCOUTs, STINs, and HGSCs. All three entities can demonstrate a consistent perturbation of genes involved in potential tumour suppressor gene silencing (EZH2), transcriptional regulation (LEF1), regulation of differentiation (RUNX2), calcium binding (RCN1), and oncogenesis (stathmin). This shared expression signature between benign and neoplastic entities links normal progenitor cell expansion to abnormal and neoplastic outgrowth in the oviduct and exposes a common pathway that could be a target for early prevention.

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Introduction

Recent discoveries have strengthened the relationship between the distal Fallopian tube and epithelial malignancies traditionally attributed to the ovary, specifically high-grade serous carcinomas (HGSCs), the most lethal of ovarian cancers [1–3]. With these discoveries has emerged a collective effort to resolve the sequence of histological and molecular events giving rise to these

tumours in the Fallopian tube. The serous carcinogenic sequence involves not only frank malignancies with metastatic spread, but also serous cancer precursors, including latent precursors – the p53 signature – and serous tubal intraepithelial neoplasms (STINs). The latter include intramucosal carcinomas (STICs) and lesser but immunophenotypically similar atypias that are considered premalignant intraepithelial lesions (STILs) [4,5]. Virtually all serous cancer precursors

contain mutations in *TP53*, evidence of a DNA damage response (γ -H2AX^P), and predominate in the distal Fallopian tube [4]. Contiguous benign (p53 signatures) and malignant (STICs) epithelia have been documented with shared mutations in specific codons of *TP53* [4,6]. In addition, further studies have unearthed other benign epithelial alterations, termed secretory cell outgrowths (SCOUTs), that do not contain *TP53* mutations or evidence of a DNA damage response, yet share with precursors and carcinomas loss of PAX2 expression [7–9]. SCOUTs do not appear directly linked to HGSC, but have been documented at higher frequency in the normal tubes of postmenopausal women and those with HGSC [8,9]. Based on these properties, we have designated SCOUTs as ‘surrogate precursors’ and hypothesize that both SCOUTs and serous cancer precursors share properties or similar mechanisms in their pathogenesis, albeit with different potential outcomes.

The shared loss of PAX2 expression in both SCOUTs and many ‘true’ serous cancer precursors suggests that inactivation of this gene, while integral to neoplasia, has a wider range of associations and may signify a generic pathway common to epithelial cell expansion. The goals of this study were, firstly, to determine the breadth of the PAX2ⁿ immunophenotype in the Fallopian tube by examining ‘normal’ cell growth and differentiation *in vitro* and *in vivo*. Secondly, we wanted to characterize more fully the alterations in expression that typified SCOUTs by array analysis and employ a biomarker

profile to determine whether the SCOUT signature was recapitulated in STINs and HGSCs.

Materials and methods

Case material

This study was approved by the Brigham and Women’s Human Investigation Committee and involved the use of discarded fresh and archived tissues. Case material for antibody staining consisted of the following epithelia/lesions: (1) normal salpingeal epithelium ($n = 15$); (2) SCOUTs ($n = 44$) and other outgrowths such as transitional-like metaplasia [Walthard cell nests (WCNs), $n = 5$]; (3) serous tubal intraepithelial neoplasms (STINs) ($n = 18$); and (4) metastatic or invasive serous carcinomas ($n = 39$). In addition, cultured clonal cells from normal Fallopian tubes were examined for selected marker expression. Cases for immunohistochemistry were selected by one of us (CPC) using previously described criteria (Figure 1) [10].

Cell culture

Fimbrial tissue was obtained from discarded surgical specimens of women undergoing benign procedures. Discarded fetal oviductal tissues were obtained by parental consent under an approved IRB protocol. Disaggregated cells were cultivated onto a feeder layer

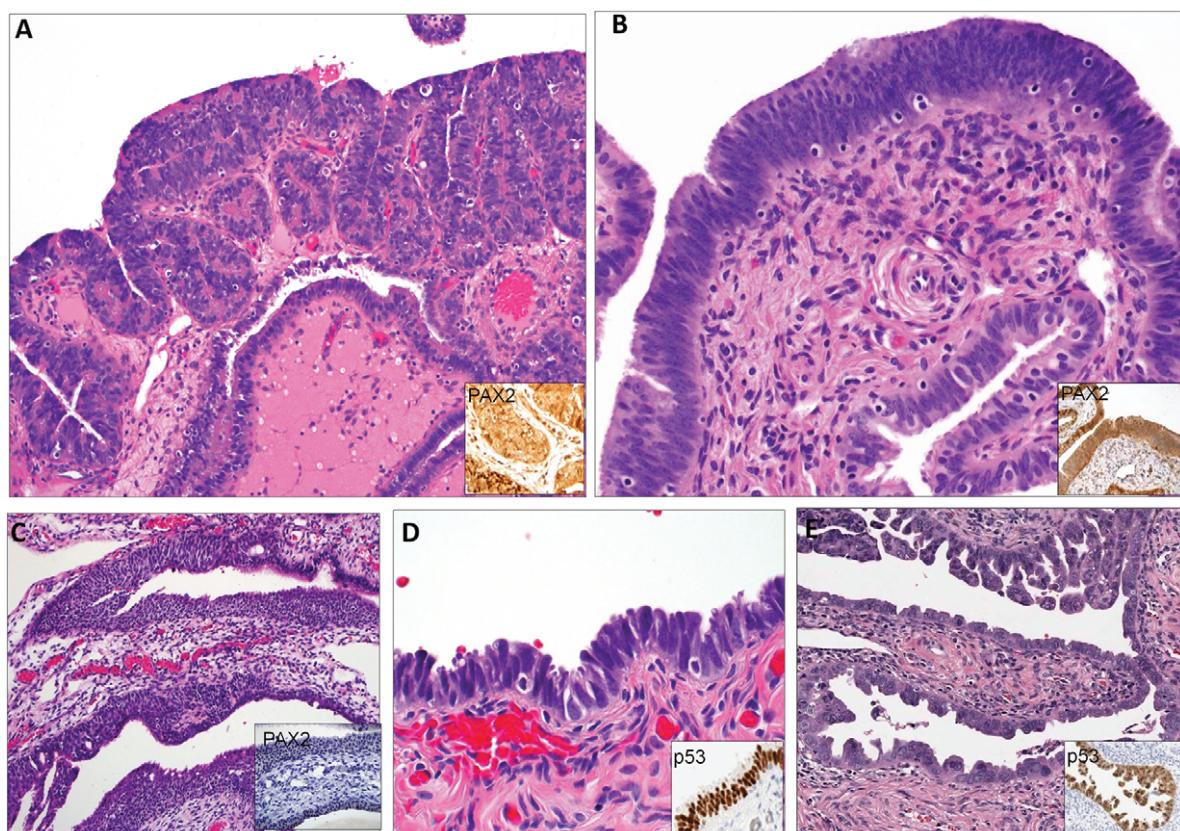


Figure 1. Entities associated with the PAX2ⁿ immunophenotype included (A) type 1 secretory cell outgrowths (SCOUTs), (B) type 2 SCOUTs, (C) Walthard cell nests, and (D) low- and (E) high- (serous tubal intraepithelial carcinoma) grade tubal intraepithelial neoplasia.

of lethally irradiated 3 T3-J2 cells in stem cell culturing media (Jackson Laboratory, scm003). Clonal analysis and *in vitro* 3D differentiation were based on previously described methods for lung epithelial stem cells [11].

Microarray and bioinformatics

In order to identify genes expressed in PAX2ⁿ epithelium, expression arrays were generated from formalin-fixed, laser-capture-micro-dissected (LCM) PAX2ⁿ SCOUTs and benign control oviductal epithelium. RNAs obtained from the LCM procedure were amplified using the Ovation FFPE WTA System, WT-Ovation Exon Module, and Encore Biotin Module (NuGEN Technologies, San Carlos, CA, USA) and hybridized onto GeneChip® Human Exon 1.0 ST Arrays. GeneChip operating software was used to process all the Cel files and calculate probe intensity values. To validate sample quality, hybridization ratios were calculated using Affymetrix Expression Console software. The intensity values were log₂-transformed and imported into the Partek Genomics Suite. Exons were summarized to genes and a one-way ANOVA was performed to identify differentially expressed genes. *p* values and fold change were calculated for each analysis. Heat maps were generated using Pearson's correlation and Ward's method with selected genes based on *p* value. Pathway analyses were performed using Gene Set Enrichment Analysis (GSEA) software. Candidate biomarkers were culled from these arrays and are summarized in Supplementary Table 1.

Immunohistochemistry

Immunostaining was performed with attention to the biomarkers in Supplementary Table 1, in which product information and dilutions are included. When normal-appearing epithelia were scanned for putative PAX2ⁿ secretory cells, sections were immunostained with two antibodies concurrently: PAX2, which stains non-ciliated cells, and FOXJ1, a ciliated cell marker. Antibodies to leukocyte common antigen (LCA) for CD3, as well as FASCIN, were also used to track intraepithelial lymphocytes and dendritic cells, which are normally PAX2ⁿ. Detection was completed with the Vectastain ABC kit (Cat No PK-6102; Vector Laboratories, Inc, Burlingame, CA, USA) with a liquid DAB-plus substrate kit (Cat No 00-2020). Slides were counterstained with Hematoxylin Stain 3 (Cat No CS402-1D). Antibody information is summarized in Supplementary Table 1. Reaction to antibody staining is indicated by superscripted 'p' or 'n' for positive or negative (PAX2, ALDH1, FOXJ1, etc), superscripted 'm' or 'wt' for mutated or wild type (p53), and superscripted 'nc' or 'mem' for nuclear and cytoplasmic versus membrane localization (β -catenin). Immunohistochemistry, immunofluorescence staining, and image acquisition were performed as previously described [9,11]. Proliferating clones were identified and immunostained for PAX2, PAX8, FOXJ1, Krt7, Krt5, p63, EZH2,

and Ki67. Evidence of ciliated cell differentiation was identified by immunostaining for FOXJ1 and acetylated alpha-tubulin. Basal cells were identified by Krt5 or p63 immunostaining.

Results

Histological sub-classification of SCOUTs and STINs

The lesions under study are illustrated in Figure 1. Based on previous studies, SCOUTs were subdivided into two general histological categories [8,12]. The first, designated as type 1 SCOUTs, consisted of a typical mono- or bi-phasic tubal epithelial composition with either single layers of tubal non-ciliated cells or (more commonly) a combination of non-ciliated and ciliated cells. The second, arbitrarily labelled type 2 SCOUTs, consisted of proliferations with mildly pseudostratified and closely arranged elongated fusiform nuclei, similar to endometrial epithelium, and also termed 'endometrioid' SCOUTs. Cells with ciliated differentiation (FOXJ1^p) were present, but were typically less than 30% of the cells and scattered throughout the epithelium. Walthard cell nests (WCNs), consisting of basal cell outgrowth with a squamo-transitional phenotype, were also studied because they signify another form of outgrowth derived from columnar epithelial cells, albeit metaplastic. STINs were sub-classified as previously described and contained strong p53 immunostaining and evidence of DNA damage by H2AX staining [5]. Those with mild or moderate atypia and preserved epithelial polarity were classified as low grade and are identical to lesions classified as 'STILs', 'TILTs', and atypical hyperplasia in other reports [13–15]. Those with conspicuous loss of epithelial polarity were classified as high grade, synonymous with serous tubal intraepithelial carcinoma (STIC). The latter have a 0–11% outcome risk of HGSC, based on recent studies [16–18]. The HGSC outcome risk of lower-grade STINs is unknown but presumed to be less than that of high-grade STINs.

In vitro and *in vivo* expression of PAX2 in the Fallopian tube mucosa

Cultured epithelial cells from the gynaecological tract, both in adults and at 20 weeks' gestation, were plated and colonies of clonogenic cells were characterized. The dominant immunophenotype associated with highly-proliferative clonogenic cell outgrowth was Krt7^p/PAX8^p/EZH2^p/ PAX2ⁿ/Krt5ⁿ/p63ⁿ (Figures 2A, 3A, and Supplementary Figure 2A). FOXJ1 expression indicating ciliated cell differentiation was also seen occasionally in the non-proliferative cells that were not stained positively with Ki67 (Figure 2A). To examine the differentiation ability of these cloned cells at the single-cell level, we established single-cell pedigree lines by subsequent rounds of plating and clone selection (Figure 2B). Pedigree lines of these cloned oviductal progenitor cells were differentiated

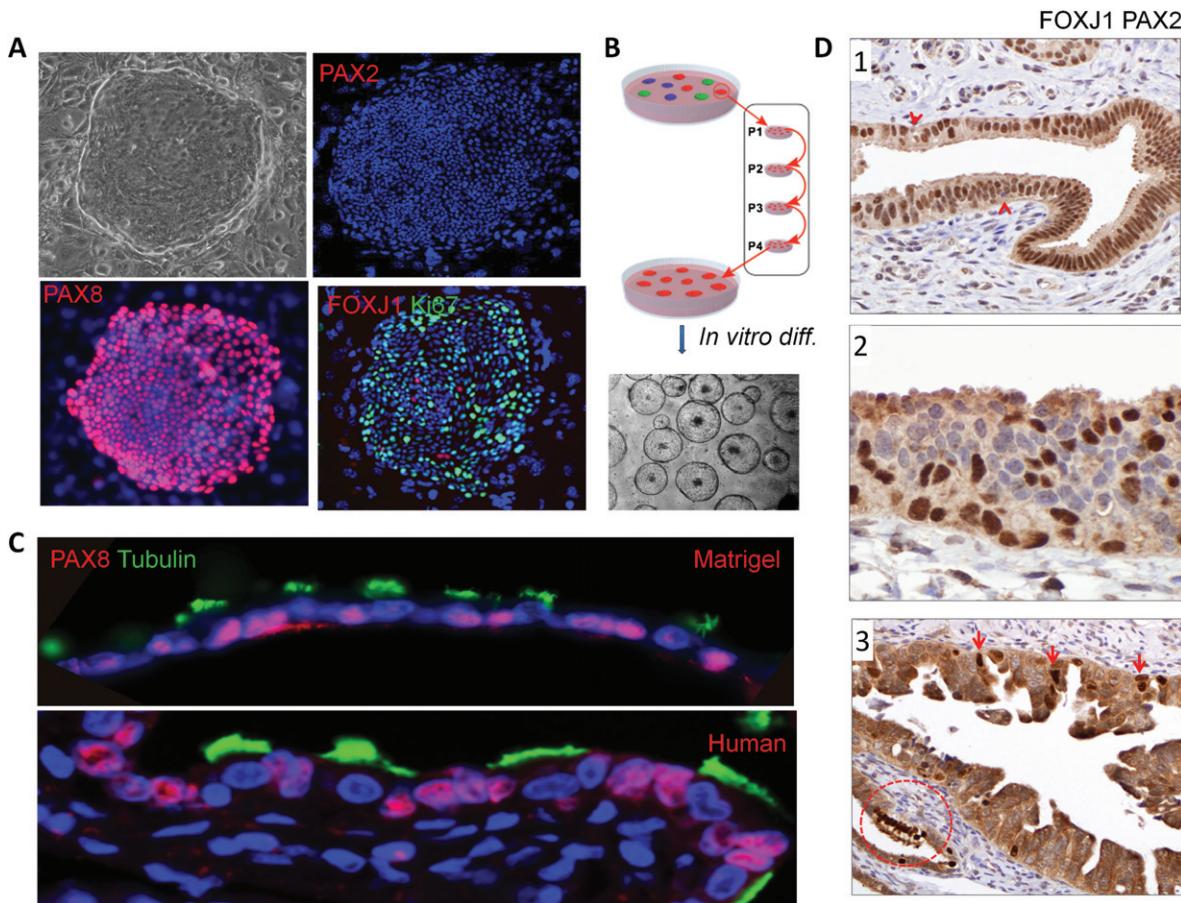


Figure 2. *In vitro* propagation and differentiation of oviductal progenitor cells. (A) The cells cloned from fetal or adult oviduct are PAX2ⁿ, PAX8^p and occasionally express differentiation marker (FOXJ1) in non-proliferative cells (Ki67⁻). (B) Schematic diagram of pedigree cell line establishment. (C) Upper panel: representative image of fetal (20-week) oviductal progenitor cells differentiated in 3D Matrigel culture system. Lower panel: immunofluorescence image of human adult oviduct epithelium. Acetyl-alpha-tubulin (green) indicates ciliated cell differentiation. PAX8 (red) indicates non-ciliated cells. DAPI stains nuclei (blue). (D1) Combined staining of histological sections of normal tube with both PAX2 and FOXJ1 reveals widespread nuclear staining, except occasional lymphocytes (arrows). (D2) Occasional foci of multi-layered epithelium undergoing ciliated cell differentiation (positive nuclei) consist of some cells negative for PAX2. (D3) Tubal intraepithelial carcinoma with focal FOXJ1 staining (arrowheads) indicating ciliated cell differentiation. Circled focus of normal ciliated cells is an internal positive control.

in either an air–liquid interface (ALI) cell culture system or 3D Matrigel cultures for 10–20 days. In 3D Matrigel cultures, PAX8^p oviductal progenitor cells differentiated into columnar epithelium consisting of acetylated tubulin^p/FOXJ1^p/PAX8ⁿ ciliated cells and PAX8^p non-ciliated cells, which resembles the human oviduct histology (Figure 2C). In the ALI culture system, a series of images of acetylated tubulin expression were taken at different time points during the differentiation and showed that the oviductal progenitor cells started to differentiate into ciliated cells at day 3 and became maturely differentiated at day 10 (Supplementary Figure 2B). At day 10 in the ALI culture system, the cloned oviductal progenitor cells formed a simple epithelium with ciliated cells marked by FOXJ1 and acetylated tubulin and non-ciliated cells marked by PAX2 (Supplementary Figure 2C). It is noteworthy that while the proliferating population is PAX2ⁿ (Figure 2A), PAX2 expression was reclaimed in some non-ciliated (secretory) cells. This further indicates that the progeny of a single oviductal progenitor cell can

give rise to all epithelial lineages typically found in the oviduct, including not only mature ciliated cells but also non-ciliated (secretory) cells.

Immunostaining of both fetal and adult Fallopian tubes was performed to ascertain the distribution of PAX2-expressing cells and address the possibility that the PAX2ⁿ immunophenotype was programmed earlier in development. Histological sections of fetal (at 21 weeks) and adult Fallopian tubes were examined. Fetal tubes contained an abundance of PAX2^p cells, with occasional interspersed ciliated cells (Supplementary Figure 1A). Expression of PAX8 was similar in distribution (Supplementary Figure 1B). Similarly, in normal adult tubes, PAX2 staining was extensive in cells that were not undergoing ciliated (tubulin^p) differentiation (Supplementary Figure 1C). A summary of immunophenotypes for progenitor and adult cells is displayed in Supplementary Table 2.

In the adult tubes, sections were also stained with FOXJ1, and/or LCA to account for other PAX2ⁿ

cells that were either undergoing ciliated differentiation or were non-epithelial. Mono-layered or mildly pseudostratified normal Fallopian tube mucosa typically contained cells expressing either PAX2 or FOXJ1 (Figure 2D1). In occasional foci of prominent multi-layered epithelium with some cells staining positive with FOXJ1, loss of PAX2 nuclear staining could be seen (Figure 2D2), giving the impression that loss of PAX2 expression in non-ciliated cells was coordinated with cell growth in multi-layered epithelium. Albeit less so, FOXJ1 staining was also seen in STINs, supporting ciliated differentiation in PAX2ⁿ neoplastic growth (Figure 2D3).

Metaplastic (WCNs) differentiation of PAX2ⁿ columnar cells *in vitro* and *in vivo*

WCNs are foci of transitional-like metaplasia in the fimbria or adjacent peritoneal surface and are emblematic of basal cell outgrowth that can develop near the junctions

of disparate epithelial types [19]. Other sites include the gastro-oesophageal and cervical squamo-columnar junctions. Both have been designated as sites harbouring residual embryonic cells and studies of the latter have suggested that basal or reserve cells emerge from the overlying columnar cells and then undergo squamous metaplasia [20,21]. This process has been termed 'top-down' differentiation, ie the progeny (basal cells) emerge from beneath the progenitor population. However, no study has ever displayed this sequence *in vitro*. Fetal tubal cells propagated *in vitro* were strongly positive for both Krt7 and PAX8, in keeping with Müllerian epithelium (Figures 2A and 3A). Moreover, these progenitor cells did not express Krt5 or p63 (Figure 3A). Interestingly, when pedigree lines of these cloned oviductal progenitor cells were differentiated in 3D Matrigel cultures for 10–20 days, in addition to the typical ciliated cell differentiation (Figure 2C), subjacent p63/Krt5^p basal cells emerged (Figure 3B1) and expanded (Figure 3B3) in a pattern similar to that

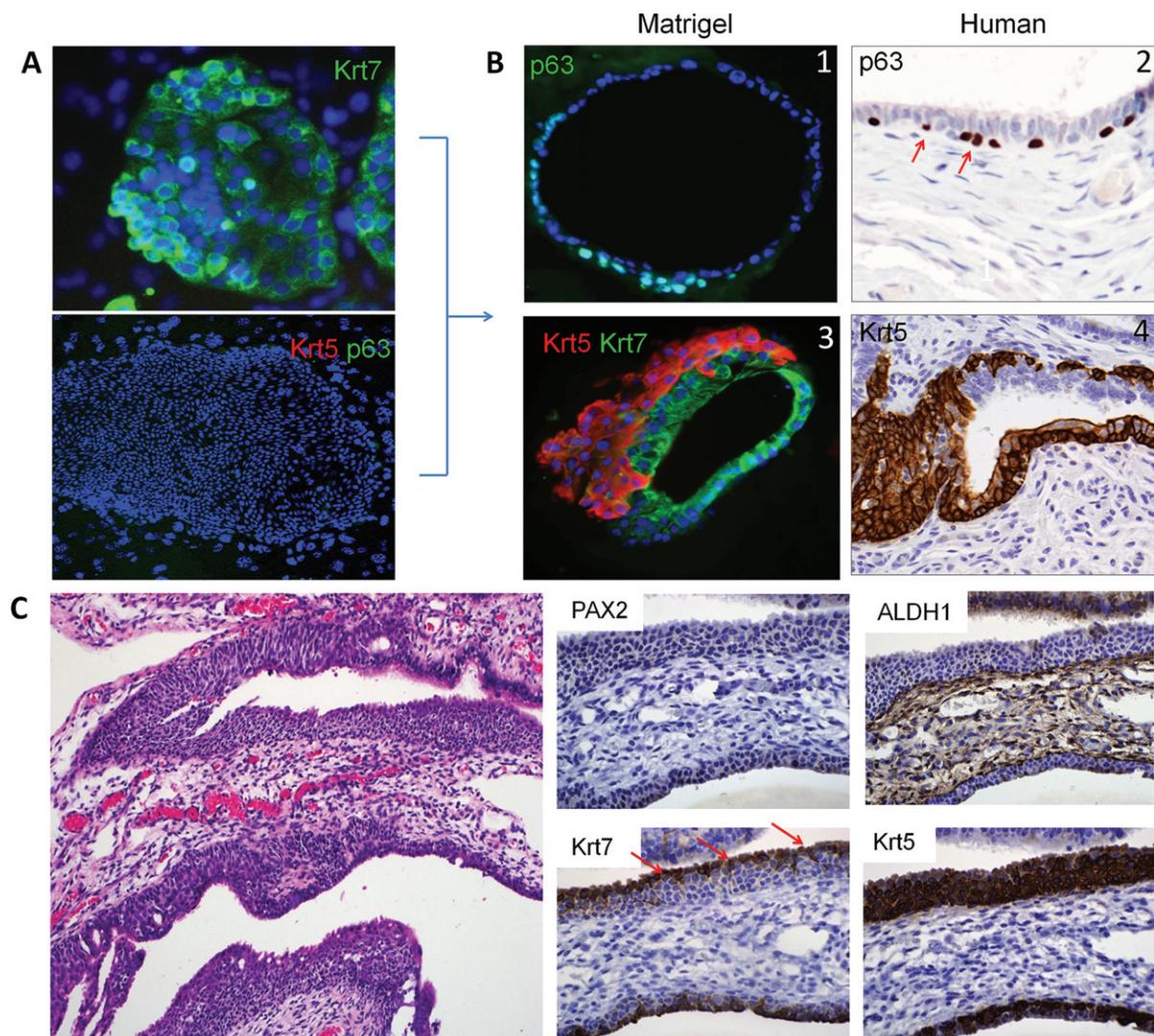


Figure 3. *In vitro* and *in vivo* basal cell differentiation in the oviduct. (A) Colonies of Krt7^p/Krt5ⁿ/p63ⁿ cells from a 20-week-old fetal oviduct. (B1, B3) Single (p63, green) and multi-layered (Krt5, red) basal cell outgrowth seen in Matrigel cultures. (B2, B4) Similar basal cell growth highlighted by p63 and Krt5 in the adult fimbria. (C) Walthard cell nest in the adult tube is typically PAX2 and ALDH1 negative. Residual Krt7-positive cells (arrows) are displaced from beneath by an expanding Krt5 population.

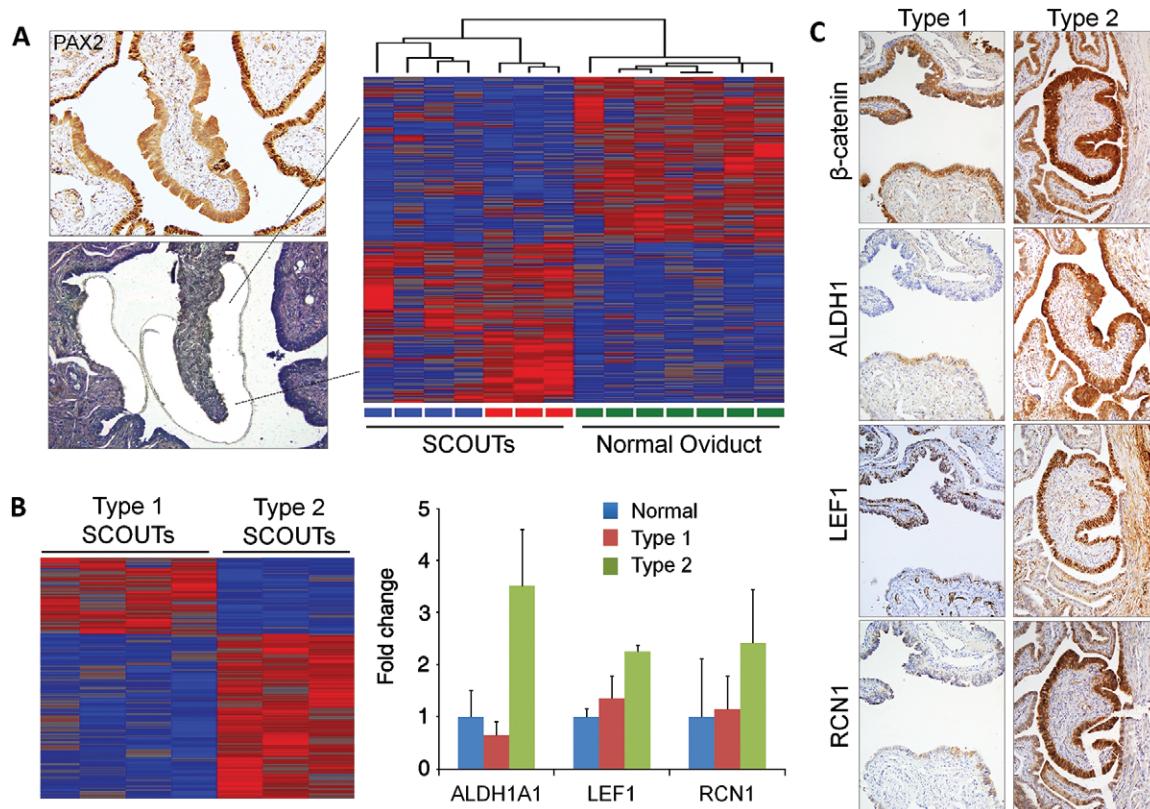


Figure 4. (A) Laser-captured micro-dissected SCOUTs (left) and a heat map comparison of SCOUTs and normal oviduct (right). (B) Arrays generated from PAX2ⁿ SCOUTs revealed genes differentially expressed across type 1 and type 2 SCOUTs, including ALDH1, LEF1, and RCN1 (right). (C) Coordinated expression of the above genes distinguish type 1 SCOUTs, which show membranous β-catenin localization and absent ALDH1 staining plus negative or weak staining for LEF1 and RCN1 staining (left), from type 2 SCOUTs, with nuclear and cytoplasmic β-catenin, strong ALDH1, LEF1, and RCN1 staining (right).

seen in p63/Krt5^p cells in WCNs in the adult tube (Figures 3B2 and 3B4). *In vitro*, the Krt5 and p63 immunopositive cells were superimposed, although the Krt5 staining index was higher (Supplementary Figure 2E). Analysis of WCNs in tissue sections (Figure 3C) revealed a strikingly similar pattern of growth and differentiation, arising either from beneath Krt7^p epithelial cells or in continuity with columnar epithelium typical of type 1 SCOUTs. The result was a PAX2ⁿ/ALDH1ⁿ transitional-like outgrowth that was strongly Krt5^p but stathminⁿ (not shown). Taken in the context of the *in vitro* findings, this observation further linked the PAX2ⁿ immunophenotype to cell outgrowth and a Krt7^p progenitor cell to the development of not only terminal (FOXJ1⁺) but also metaplastic (Krt5⁺) differentiation in the Fallopian tube.

Altered gene expression in PAX2ⁿ proliferations (SCOUTs, STINs, and HGSCs)

Supplementary Table 3 is a list of genes selected for analysis and found to be differentially expressed in SCOUTs relative to normal-appearing epithelium. Arrays generated from RNA extracted from formalin-fixed laser-capture micro-dissected SCOUTs yielded differentially expressed genes, illustrated in the representative heat map (Figures 4A, 4B, and Supplementary Figures 4 and 5). When stained with selected

markers, type 1 SCOUTs varied from strictly secretory to mixed secretory and ciliated, and were ALDH1ⁿ, β-catenin^{mem} and stained weakly or negative for LEF1, RCN1, RUNX2, and EZH2 (Figures 4C, 5, and Supplementary Figure 3). Type 2 SCOUTs stained variably for ciliated cell differentiation and were β-catenin^{nc} and ALDH1, LEF1, RCN1, EZH2, RUNX2 (not shown) and stathmin positive (Figures 4C, 5, and Supplementary Figure 3). Basal cell differentiation, signifying WCN development, was associated with PAX2ⁿ columnar epithelium, suggesting that this pathway of differentiation might initiate within type 1 PAX2ⁿ SCOUTs.

Figure 5 and Supplementary Figure 6 summarize the staining patterns observed in the different lesions. STINs and HGSCs shared expression of several markers with SCOUTs. Expression patterns for ALDH and β-catenin were identical to type 1 SCOUTs (ALDHⁿ and β-catenin^{mem}). In addition, like type 2 SCOUTs, there was increased staining for EZH2, stathmin, LEF1, RCN, Krt5, and RUNX2 (not shown). Not surprisingly, no marker in this group separated STINs or HGSCs from SCOUTs. This is in contrast to other published markers such as Ki67, cyclin E, p16, and others, which are significantly more commonly expressed in STINs and HGSCs relative to benign Fallopian tube mucosa [4,5,15,22].

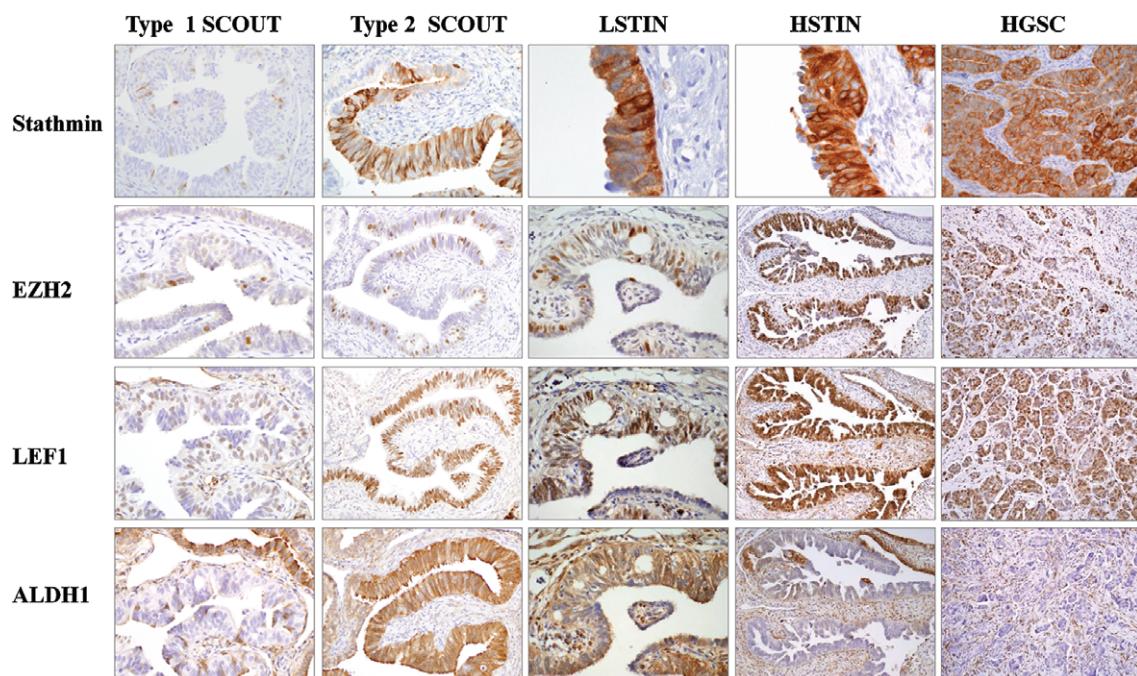


Figure 5. Shared expression of SCOUT markers with low- (LSTIN) and high- (HSTIN or STIC) grade serous tubal intraepithelial neoplasia and high-grade serous carcinoma (HGSC). Neoplasms (STINs, HGSCs) share with type 1 SCOUTs loss of PAX2 and ALDH1, and with type 2 SCOUTs, increased LEF1, EZH2, and stathmin and other markers (see text).

Discussion

Analysis of arrays generated from high-grade serous cancer has confirmed a transcriptome that parallels oviductal epithelium [23]. Given that these tumours are strongly positive for biomarkers (such as PAX8) typically assigned to non-ciliated (so-called secretory) cells, the assumption has been that the secretory cell is the cell of origin [1]. Levanon *et al* showed that PAX8-expressing (secretory) cells of the tube were uniquely susceptible to DNA damage imposed by irradiation, a finding that parallels similar observations in latent precursors (p53 signatures) and STINs that contain p53 mutations [5,24]. However, with the discovery of PAX2ⁿ SCOUTs and a similar PAX2ⁿ expression pattern in many STINs, it became clear that there may be a relationship between the two entities, despite the fact that SCOUTs are more ubiquitous in the Fallopian tube and do not arise in the setting of a DNA damage response and loss of p53 function. Although altered PAX2 expression has been associated with neoplasia, we hypothesized that the PAX2ⁿ immunophenotype typified a 'generic' series of molecular events that were the underpinning of stem cell expansion common to many proliferations.

We addressed PAX2 expression or loss in the Fallopian tube from three perspectives. The first was by analysing expression and differentiation in proliferating normal adult and fetal cells propagated *in vitro*. The second was by comparing the *in vitro* findings to expression in tissue sections from fetal and adult tubes. The third was to look for shared expression across PAX2ⁿ cells in cell proliferation and expansion (SCOUTs,

STINs, and HGSCs). We discovered that the PAX2ⁿ immunophenotype was particularly linked to *in vitro* and *in vivo* cell growth, not infrequently with an increase in EZH2 expression. Moreover, in highly clonogenic Krt7^p/FOXJ1ⁿ oviductal progenitor cells grown *in vitro*, we demonstrated for the first time that PAX2ⁿ expanding populations were capable of both ciliated (FOXJ1) and basal cell (Krt5) differentiation. This sequence of cell growth and differentiation was recapitulated in SCOUTs, STINs, and HGSCs, with progressively reduced ciliated differentiation in the type 2 SCOUTs, STINs, and HGSCs. We thus concluded that all of these entities were related to a similar progenitor cell.

The next goal was to determine if the cells involved in benign and neoplastic outgrowth shared common expression patterns and we chose to use the least proliferative lesions (SCOUTs) as the reference. One advantage of this approach is to identify events that occur prior to the more dramatic molecular changes that characterize malignancy that may have profound influences on expression. The study delineated two general groups of SCOUTs: the first (type 1) closely resembled normal tubal epithelium, histologically and in their expression profile (Figure 1D). The second (type 2) was composed of proliferations with less pronounced ciliated differentiation, many noticeably 'endometrial'-like (Figure 1E). Accordingly, there was minimal difference in expression between type 1 SCOUTs and control epithelium, although they were consistently ALDH1ⁿ. In contrast, type 2 SCOUTs demonstrated nuclear and cytoplasmic β -catenin staining plus increased BCL2 (see ref 7), ALDH1, and Krt5 staining. This diversity in phenotype underscores the complexity of cell growth

and differentiation that can occur in the Fallopian tubes with age. Type 1 SCOUTs appear to signify very minor genomic changes, as evidenced by the similarities in transcription to normal controls. Thus, the alterations in transcription are limited to absence of ALDH1 expression. In contrast, type 2 SCOUTs, which exhibit a more divergent histology, have a common biomarker signature – stathmin, EZH2, LEF1, RCN1, and RUNX2 – that is more similar to premalignant (STINs) and malignant (HGSCs) entities in the tube (Figure 5).

A fundamental question stemming from the above observation is the relevance of the gene signature found in SCOUTs, STINs, and HGSCs to both stem cell biology and neoplasia. ALDH1 has been identified as a marker of epithelial stem cells. Its expression can be both increased or absent, the latter more typical of STINs and HGSCs [25,26]. EZH2 is a polycomb suppressor that is implicated in stem cell maintenance and regulation of differentiation. It is noteworthy that EZH2 expression typically increased in areas of cell expansion, in keeping with the coordinated suppression of PAX2 expression [27]. EZH2 is also a potential suppressor of tumour suppressor genes [28]. LEF1 is likewise expressed during lineage differentiation [29]. The function of RCN1 is less clear but this gene product is a calcium binder that is weakly expressed in renal tubular cells and up-regulated in renal cell carcinomas [30]. RUNX2 is a gene involved in morphogenesis and osteoblastic differentiation [31]. Functions attributed to stathmin are multiple. It is a marker of P13 kinase

activation that has been linked to serous neoplasia in some studies, tumour progression and metastases in others, and regulates p53 stability in still others [32–34]. Its range of expression, including normal epithelium, SCOUTs, and STINs, is similar to that of these other markers, several of which (ALDH1, PAX2, EZH2) have also been linked to not only stem cells but also outcome or resistance to chemotherapy [35–37]. The significance of the unique β -catenin staining in type 2 SCOUTs, with a shift in distribution from the membrane to the cytoplasm and nucleus, is unclear but it is emblematic of Wnt pathway activation, and mutations in β -catenin are commonly found in endometrial and colon carcinomas [38].

Walthard cell nests are a common benign condition seen in the distal Fallopian tube mucosa or the adjacent peritoneal reflection [19]. They bear a close resemblance to the cervical squamo-columnar junction, where columnar cells are undermined by p63-positive basal cells. These cells could be envisioned to either originate from the columnar epithelium or give rise to the overlying Krt7-positive epithelial cells. This study has made two novel observations. First, based on the Matrigel cell culture data, the basal cells emerge from the Krt7-positive columnar cells. Second, this process is marked by not only loss of PAX2 but also ALDH1 expression, similar to that seen in type 1 SCOUTs. The initiating cell, the Krt7^p non-ciliated epithelial cell, is remarkably similar to the cells seen in the squamo-columnar (SC) junction of the cervix from which squamous metaplasia is derived and this process is similar to so-called ‘top-down’ differentiation reported in the SC junction [21]. The fact that

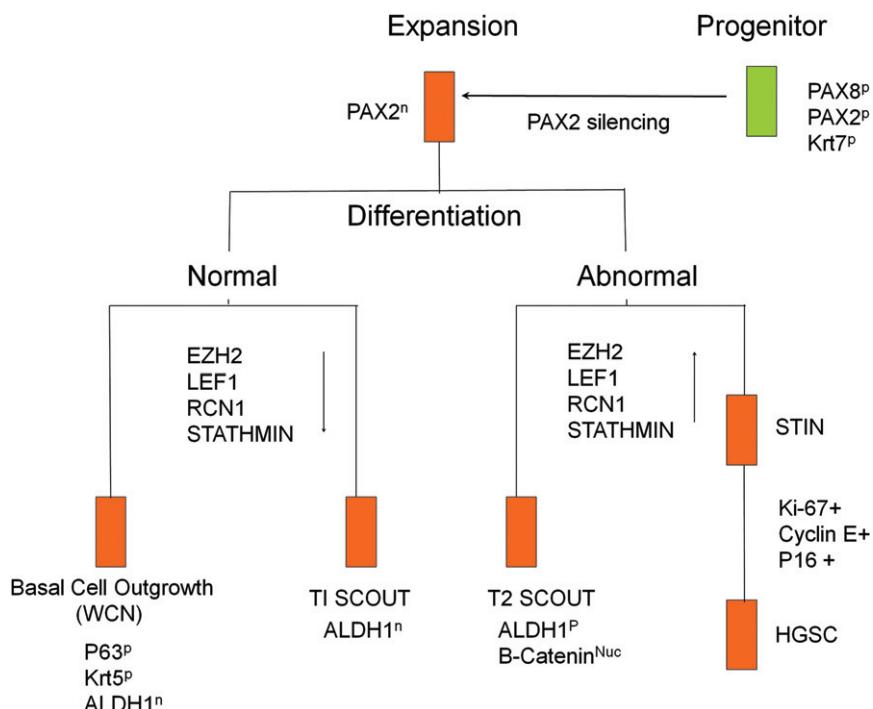


Figure 6. A progenitor cell model for the Fallopian tube in which Krt7 identifies the progenitor cell and PAX2ⁿ defines progenitor cell expansion. Expanding PAX2ⁿ cells can differentiate into basal or ciliated cells in WCNs or type 1 SCOUTs, both of which approximate normal differentiation pathways, with loss of ALDH1 and normal or minimally increased expression of LEF1, RCN1, stathmin, and EZH2. In contrast, type 2 SCOUTs and STINs (right) share a different expression signature characterized by multiple genes, including EZH2, LEF1, RCN1, and stathmin and others, involved in a divergent pathway of progenitor cell growth.

WCNs are not considered direct precursors to malignancy is not surprising, in as much as they are terminally differentiated relative to their progenitors. This is similar to the cervix, where the progenitor cells in the SC junction are considered more vulnerable to neoplastic transformation than their metaplastic progeny [21]. What is interesting is the fact that WCNs underscore the existence of multi-potential cells in the distal Fallopian tube [12]. Given that 40–60% of HGSCs do not have a documented source (or STIN) in the Fallopian tube mucosa, coupled with the fact that a subset of HGSCs are strongly Krt5-positive, the possibility that cells involved in alternate differentiation pathways might contribute to a subset of these malignancies deserves further study (Hanamornroongruang S, Howitt BE, Crum CP, unpublished) [5,25].

Epithelia in virtually every organ (breast being a prime example) display a wide range of clonal expansions, some of which may be direct precursors to malignancy and others of which serve as risk factors for a malignant outcome. The model depicted in Figure 6 reflects a similar but novel scenario in the oviduct, with multiple categories of putative monoclonal cell outgrowth and striking similarities in expression across multiple genes between surrogate precursors and lesions that are considered premalignant or pre-metastatic. These findings emphasize the complexity of molecular and phenotypic perturbations that can take place in the Fallopian tubes during and following menopause. This complexity invites caution when considering the role (or diagnostic value) of newly discovered biomarkers as specific indicators of neoplasia. More importantly, it reveals a consistent disturbance in progenitor cell biology in keeping with a common pathway that is triggered by more than one initiating event. Thus, it introduces two approaches to cancer prevention, one directed at the initiating event and the other at the early perturbations in the pathway.

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Author contribution statement

Contributions of the co-authors to design (1), data collection (2), data analysis (3), data interpretation (4), literature search (5), figures (6), and manuscript writing (7)

were as follows: GN (1–4, 6, 7); JGB (1–4, 6, 7); YY (1–3, 6); XW (2, 3); BEH (1, 2, 4, 5); MH (1–4); EY (1–3, 5); YH (2–4); MC (2–4); LW (2–4); SH (2–4); FDMcK (1, 4, 7); CPCr (1, 4, 7); and WX (1, 3, 4, 7).

Abbreviations

ALI, air–liquid interface culture; SCOUT, secretory cell outgrowth; STIN, serous tubal intraepithelial neoplasia; WCN, Walthard cell nest

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SUPPORTING INFORMATION ON THE INTERNET

The following supporting information may be found in the online version of this article:

Figure S1. Pax2 and acetyl-alpha-tubulin (cilia) expression in fetal and adult Fallopian tubes.

Figure S2. *In vitro* differentiation of oviduct progenitor cells.

Figure S3. Two types of PAX2^{hi} SCOUTs are distinguished in these panels with β -catenin, keratin 5, and LEF1 staining.

Figure S4. Heat map comparing type 1 and type 2 SCOUTs with normal tubal epithelium and high-grade serous cancer.

Figure S5. A depiction, in tabular (A) and graphical format (B), of genes up-regulated with the two-fold change in type 2 relative to type 1 SCOUTs, several of which have been linked to STIN and HGSC.

Figure S6. H&E, p53, and PAX2 staining of cases under study (see Figure 5).

Table S1. Biomarkers selected for analysis of clonogenic cells, SCOUTs, and STINs.

Table S2. Summary of immunophenotypes in cultured progenitor cells and adult cells in tissue sections.

Table S3. Upregulated genes in Type 2 SCOUTs in comparison with Type 1 SCOUTs (3 fold and $p < 0.05$).